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Om protein - protein search, using sw model

Run on: April 2, 2003, 14:48:15 ; Search time 28 seconds^{*}

Scoring table: BLOSUM62

Searched: Gapext 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/aa/5A_COMB.pep;*
2: /cgn2_6/ptodata/1/aa/5B_COMB.pep;*
3: /cgn2_6/ptodata/1/aa/6A_COMB.pep;*
4: /cgn2_6/ptodata/1/aa/6B_COMB.pep;*
5: /cgn2_6/ptodata/1/aa/PCITS_COMB.pep;*
6: /cgn2_6/ptodata/1/aa/backfiles1.Pep;*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1368	100.0	257	4 US-08-050-132A-2
2	1336.5	97.7	428	1 US-08-050-132A-2
3	1336.5	97.7	428	3 US-08-750-222A-2
4	1336.5	97.7	428	3 US-08-815-652B-2
5	1336.5	97.7	428	4 US-08-254-553A-2
6	1336.5	97.7	428	5 PCT-US95-07084-2
7	1336.5	97.7	428	5 PCT-US95-07084-2
8	808.5	59.1	427	4 US-08-065-844A-2
9	808.5	46.3	150	1 US-08-050-132A-9
10	634	46.3	150	3 US-08-750-222A-9
11	634	46.3	150	3 US-08-815-652B-9
12	634	46.3	150	4 US-08-254-553A-9
13	634	46.3	150	5 PCT-US92-05374A-9
14	634	46.3	150	5 PCT-US95-07084-2
15	519.5	38.0	312	1 US-08-247-908A-2
16	519.5	38.0	312	1 US-08-453-942-2
17	519.5	38.0	312	2 PCT-US94-05390-2
18	519.5	38.0	312	5 PCT-US94-05390-2
19	516.5	37.8	424	1 US-08-247-908A-11
20	516.5	37.8	424	1 US-08-453-942-11
21	516.5	37.8	424	2 US-08-226-885A-11
22	516.5	37.8	424	5 PCT-US94-05390-11
23	469	34.3	103	1 US-08-335-553C-53
24	469	34.3	103	3 US-08-478-037A-15
25	469	34.3	103	4 US-08-931-888E-168
26	469	34.3	103	4 US-08-981-739-168
27	34.3	262574	262574	US-09-128-026-168

RESULT 1-844A-9

Sequence 9, Application US/0806584A

PATENT NO. 6333168

GENERAL INFORMATION:

APPLICANT: Jessell, Thomas M.

APPLICANT: Basler, Konrad

APPLICANT: Tomoda, Yoshia

TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: United States of America

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/065,844A

FILING DATE: 19930520

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 2B:678

REFERENCE/DOCKET NUMBER: 0576/40314

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEFAX: 422523 COOP UT

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-065-844A-9

Query Match 100.0%; Score 1368; DB 4; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.5e-131; Length 257;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 1, Appli

Sequence 2, Appli

Sequence 3, Appli

Sequence 4, Appli

Sequence 5, Appli

Sequence 6, Appli

Sequence 7, Appli

Sequence 8, Appli

Sequence 9, Appli

Sequence 10, Appli

Sequence 11, Appli

Sequence 12, Appli

Sequence 13, Appli

Sequence 14, Appli

Sequence 15, Appli

Sequence 16, Appli

Sequence 17, Appli

Sequence 18, Appli

Sequence 19, Appli

Sequence 20, Appli

Sequence 21, Appli

Sequence 22, Appli

Sequence 23, Appli

Sequence 24, Appli

Sequence 25, Appli

Sequence 26, Appli

Sequence 27, Appli

Sequence 28, Appli

Sequence 29, Appli

Sequence 30, Appli

Sequence 31, Appli

Sequence 32, Appli

Sequence 33, Appli

Sequence 34, Appli

Sequence 35, Appli

Sequence 36, Appli

Sequence 37, Appli

Sequence 38, Appli

Sequence 39, Appli

Sequence 40, Appli

Sequence 41, Appli

Sequence 42, Appli

Sequence 43, Appli

Sequence 44, Appli

Sequence 45, Appli

QY 1 DVLEDSETWDQATGSKTKFLYSLVSDQRIDEGWETLEVSAYKRAVRAADSTNNKLETVOSH 60
 Db 1 DVLEDSETWDQATGSKTKFLYSLVSDQRIDEGWETLEVSAYKRAVRAADSTNNKLETVOSH 60
 QY 61 RESC0TLDISVPPSKNLFFVVFSNDRSNGTKRTRDLKLEMIGHEQEMLVLVAKNAY 120
 Db 61 RESC0TLDISVPPSKNLFFVVFSNDRSNGTKRTRDLKLEMIGHEQEMLVLVAKNAY 120
 QY 121 OGAGESQEERGL3YTAVGPLLARRKRSTGASSHCQTSLSRVLNFEDIGWDSWITAPKEYD 180
 Db 121 OGAGESQEERGL3YTAVGPLLARRKRSTGASSHCQTSLSRVLNFEDIGWDSWITAPKEYD 180
 QY 181 AYECKGGCFPLADDVTPTRKHAIVQTLVHLKPFKVKACCVPTKLSPISPISILYKDMGV 240
 Db 181 AYECKGGCFPLADDVTPTRKHAIVQTLVHLKPFKVKACCVPTKLSPISPISILYKDMGV 240
 QY 241 TLYKHYEGMSVAECGCR 257
 Db 241 TLYKHYEGMSVAECGCR 257

RESULT 2
 US-08-050-132A-2
 Sequence 2, Application US/08050132A
 Patent No. 5561007
 GENERAL INFORMATION:
 APPLICANT: Worney, John M.
 APPLICANT: Celeste, Anthony J.
 TITLE OF INVENTION: BMP-9 COMPOSITIONS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Genetics Institute, Inc.
 STREET: Legal Affairs - 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: US
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/050,132A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kapinos, Ellen J.
 REGISTRATION NUMBER: 32,245
 REFERENCE/DOCKET NUMBER: GI 5186A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-1170
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 428 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-050-132A-2

Query Match 97.7%; Score 1336.5; DB 1; Length 428;
 Best Local Similarity 98.4%; Pred. No. 5.2e-128;
 Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DVLEDSETWDQATGSKTKFLYSLVSDQRIDEGWETLEVSAYKRAVRAADSTNNKLETVOSH 60
 Db 173 DVLEDSETWDQATGSKTKFLYSLVSDQRIDEGWETLEVSAYKRAVRAADSTNNKLETVOSH 60
 QY 61 RESC0TLDISVPPSKNLFFVVFSNDRSNGTKRTRDLKLEMIGHEQEMLVLVAKNAY 120
 Db 61 RESC0TLDISVPPSKNLFFVVFSNDRSNGTKRTRDLKLEMIGHEQEMLVLVAKNAY 120
 QY 121 OGAGESQEERGL3YTAVGPLLARRKRSTGASSHCQTSLSRVLNFEDIGWDSWITAPKEYD 180
 Db 121 OGAGESQEERGL3YTAVGPLLARRKRSTGASSHCQTSLSRVLNFEDIGWDSWITAPKEYD 180
 QY 181 AYECKGGCFPLADDVTPTRKHAIVQTLVHLKPFKVKACCVPTKLSPISPISILYKDMGV 240
 Db 352 AYECKGGCFPLADDVTPTRKHAIVQTLVHLKPFKVKACCVPTKLSPISPISILYKDMGV 411
 QY 241 TLYKHYEGMSVAECGCR 257
 Db 412 TLYKHYEGMSVAECGCR 428

RESULT 3
 US-08-750-222A-2
 Sequence 2, Application US/08750222A
 Patent No. 6034061
 GENERAL INFORMATION:
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Worney, John M.
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Song, Jeffrey
 APPLICANT: Thies, Scott
 TITLE OF INVENTION: BMP-9 COMPOSITIONS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Genetics Institute, Inc.
 STREET: Legal Affairs - 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: US
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,222A
 FILING DATE: 04 DEC 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/254, 353
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kapinos, Ellen J.
 REGISTRATION NUMBER: 32,245
 REFERENCE/DOCKET NUMBER: GI 5186B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-1170
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 428 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-750-222A-2

Query Match 97.7%; Score 1336.5; DB 3; Length 428;
 Best Local Similarity 98.4%; Pred. No. 5.2e-128;
 Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DVLEDSETWDQATGSKTKFLYSLVSDQRIDEGWETLEVSAYKRAVRAADSTNNKLETVOSH 60
 Db 173 DVLEDSETWDQATGSKTKFLYSLVSDQRIDEGWETLEVSAYKRAVRAADSTNNKLETVOSH 60
 QY 61 RESC0TLDISVPPSKNLFFVVFSNDRSNGTKRTRDLKLEMIGHEQEMLVLVAKNAY 120
 Db 61 RESC0TLDISVPPSKNLFFVVFSNDRSNGTKRTRDLKLEMIGHEQEMLVLVAKNAY 120
 QY 121 OGAGESQEERGL3YTAVGPLLARRKRSTGASSHCQTSLSRVLNFEDIGWDSWITAPKEYD 180
 Db 121 OGAGESQEERGL3YTAVGPLLARRKRSTGASSHCQTSLSRVLNFEDIGWDSWITAPKEYD 180

Db 292 QVAGESQEEGLDGTYAVGPLLARRKRSTGASSHCQKTSLRVNFDIGMSWITAPKEYD 351
 Qy 181 AYECKGCCFPPLADDVPTKHAIVQTVLWHKFPTRKGKACCVPKLSPISILYKDDMGPV 240
 Db 352 AYECKGCCFPPLADDVPTKHAIVQTVLWHKFPTRKGKACCVPKLSPISILYKDDMGPV 411
 Qy 241 TLKYHYEGMSVACGCR 257
 Db 412 TLKYHYEGMSVACGCR 428
 ;
 RESULT 4
 US-08-815-652B-2
 ; Sequence 2, Application US/08815652B
 ; Patent No. 603462
 ; GENERAL INFORMATION:
 ; APPLICANT: Wozney, John M.
 ; APPLICANT: Celeste, Anthony
 ; APPLICANT: Song, Jeffrey
 ; APPLICANT: Thies, R. Scott
 ; TITLE OF INVENTION: BMP-9 COMPOSITIONS
 ; NUMBER OF SEQUENCES: 19
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: Legal Affairs - 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02140
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/815,652B
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kapinos, Ellen J.
 ; REGISTRATION NUMBER: 32,245
 ; REFERENCE/DOCKET NUMBER: GI 5186D
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 876-1170
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 428 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-815-652B-2
 ;
 ; Query Match 97.7%; Score 1336.5; DB 3; Length 428;
 ; Best Local Similarity 98.4%; Pred. No. 5.2e-128; Gaps 1;
 ; Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
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 Qy 1 DVLEDSEWWDQATGKTFLVSQDIRDGWETLEVSAAKVRVRAADSTNNKLETVQSH 60
 Db 173 DVLEDSEWWDQATGKTFLVSQDIRDGWETLEVSAAKVRVRAADSTNNKLETVQSH 232
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 Qy 61 RESCDLDSVPPGSKNLPFFVFSNDRSNGTKEPLDILKEMIGHEQETMVKTAKEY 120
 Db 233 RESCDLDSVPPGSKNLPFFVFSNDRSNGTKEPLDILKEMIGHEQETMVKTAKEY 291
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 Qy 121 QGAGESQEEGLDGTYAVGPLLARRKRSTGASSHCQKTSLRVNFDIGMSWITAPKEYD 180
 Db 292 QVAGESQEEGLDGTYAVGPLLARRKRSTGASSHCQKTSLRVNFDIGMSWITAPKEYD 351
 ;
 Qy 181 AYECKGCCFPPLADDVPTKHAIVQTVLWHKFPTRKGKACCVPKLSPISILYKDDMGPV 240
 Db 352 AYECKGCCFPPLADDVPTKHAIVQTVLWHKFPTRKGKACCVPKLSPISILYKDDMGPV 411
 ;
 Db 412 TLKYHYEGMSVACGCR 257
 ;
 ; RESULT 5
 US-08-254-353A-2
 ; Sequence 2, Application US/08254353A
 ; Patent No. 6287816
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Vicki A.
 ; APPLICANT: Wozney, John M.
 ; APPLICANT: Celeste, Anthony J.
 ; APPLICANT: Song, Jeffrey
 ; APPLICANT: Thies, Scott
 ; TITLE OF INVENTION: BMP-9 COMPOSITIONS
 ; NUMBER OF SEQUENCES: 19
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: Legal Affairs - 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02140
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/254,353A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kapinos, Ellen J.
 ; REGISTRATION NUMBER: 32,245
 ; REFERENCE/DOCKET NUMBER: GI 5186B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 876-1170
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 428 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-254-353A-2
 ;
 ; Query Match 97.7%; Score 1336.5; DB 4; Length 428;
 ; Best Local Similarity 98.4%; Pred. No. 5.2e-128; Gaps 1;
 ; Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 ;
 Qy 1 DVLEDSEWWDQATGKTFLVSQDIRDGWETLEVSAAKVRVRAADSTNNKLETVQSH 60
 Db 173 DVLEDSEWWDQATGKTFLVSQDIRDGWETLEVSAAKVRVRAADSTNNKLETVQSH 232
 ;
 Qy 61 RESCDLDSVPPGSKNLPFFVFSNDRSNGTKEPLDILKEMIGHEQETMVKTAKEY 120
 Db 233 RESCDLDSVPPGSKNLPFFVFSNDRSNGTKEPLDILKEMIGHEQETMVKTAKEY 291
 ;
 Qy 121 QGAGESQEEGLDGTYAVGPLLARRKRSTGASSHCQKTSLRVNFDIGMSWITAPKEYD 180
 Db 292 QVAGESQEEGLDGTYAVGPLLARRKRSTGASSHCQKTSLRVNFDIGMSWITAPKEYD 351
 ;
 Qy 181 AYECKGCCFPPLADDVPTKHAIVQTVLWHKFPTRKGKACCVPKLSPISILYKDDMGPV 240
 Db 352 AYECKGCCFPPLADDVPTKHAIVQTVLWHKFPTRKGKACCVPKLSPISILYKDDMGPV 411
 ;
 Db 412 TLKYHYEGMSVACGCR 257
 ;

RESULT 6
PCT-US92-05374A-2
; Sequence 2, Application PC/TUS9205374A

GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
ZIP: 02140

ADDRESS: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05374A
FILING DATE: 19920625

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1110
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US92-05374A-2

Query Match 97.7%; Score 1336.5; DB 5; Length 428;
Best Local Similarity 98.4%; Pred. No. 5.2e-128;
Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DVLEDSETWDQATGKFLVSDIDREGWETLEVASAVKWRADSTTNKNLKETVOSH 60
Db 173 DVLEDSETWDQATGKFLVSDIDREGWETLEVASAVKWRADSTTNKNLKETVOSH 232

Qy 61 RESCDTLDISVPPGSKNLIPFFVFSNDRSNGTKEERIDLKEMGHEQETMVLAKHAY 120
Db 233 RESCDTLDISVPPGSKNLIPFFVFSNDRSNGTKEERIDLKEMGHEQETMVLAKHAY 291

Qy 121 QGAGESQEREGLQTYAVGPLARRKRSTGASSHQCQTSLRVNFEDIGMSWITAKHAY 180
Db 292 QGAGESQEREGLQTYAVGPLARRKRSTGASSHQCQTSLRVNFEDIGMSWITAKHAY 351

Qy 181 AYECKGGCFPLADDVPTKHAIVQTLVHLKEPTKVGKACCVPLSPSILYKDDMGP 240
Db 352 AYECKGGCFPLADDVPTKHAIVQTLVHLKEPTKVGKACCVPLSPSILYKDDMGP 411

Db 292 QWADQSQEREGLQTYAVGPLARRKRSTGASSHQCQTSLRVNFEDIGMSWITAKHAYD 351

Qy 181 AYECKGGCFPLADDVPTKHAIVQTLVHLKEPTKVGKACCVPLSPSILYKDDMGP 240
Db 352 AYECKGGCFPLADDVPTKHAIVQTLVHLKEPTKVGKACCVPLSPSILYKDDMGP 411

Qy 241 TLKYHEGMSVAEGCR 257
Db 412 TLKYHEGMSVAEGCR 428

RESULT 7
PCT-US95-07084-2
; Sequence 2, Application PC/TUS9507084
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9

RESULT 8
US-08-065-844A-2
; Sequence 2, Application US/08065844A
GENERAL INFORMATION:
APPLICANT: Jessel, Thomas M.
APPLICANT: Basler, Konrad
APPLICANT: Yonada, Toshiya
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF
TITLE OF INVENTION: DORSALIN-1
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America

ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 19930520
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28, 678
 REFERENCE/DOCKET NUMBER: US/08/065,844A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9350
 TELEFAX: (212) 664-0525
 TELEX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 427 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-065-844A-2

Query Match 59.1%; Score 808.5; DB 4; Length 427;
 Best Local Similarity 61.9%; Pred. No. 3.4e-74;
 Matches 161; Conservative 31; Mismatches 59; Indels 9; Gaps 5;

QY 1 DVLDELDSETWDQAGTKFLVSDPDIRDEGWETLEVSAAKWRADSTINKNKLLEVTHOSH 60
 Db 174 DVL-DGGDHWENKENKSTKLSSVLSIODOGSHMPEWENSAVAKRNKADKMKTKLNKLEVIESK 232

QY 61 RES--CPIQDLSVSPPKNLPEFVIFNSDRNSNGKETRDLKEMIGEQQEMMLWTK 117
 Db 233 DLSGFPCCGKLDITVTHDKNPLILTVFSNDRSNGKETRDLKEMIGEQQEMMLWTK 291

QY 118 NAVOCAGESQEQEGLDGTAVGPPLARRKSTGASSHCQKSLRVNFEDIGWDSWITAPK 177
 Db 292 NDSSSEEDQREEKAI--ARRQHRSRSKSIGA-NHCRITSLVNFKEIGWMSWITAPK 347

QY 178 EYDAVECKGGCFPLADDVTPKTHAVQTLVHLKPPTKVKAACVPTKLSPLSILYKDM 237
 Db 348 DYEAFECKGCFPLDNTVTPKTHAVQTLVHLQNPKKASKACVPTKLDASILYKDA 407

QY 238 GVTPLTKYHVEGMSVAECOCR 257
 Db 408 GVTPLIYVHEGMSVAECOCR 427

RESULT 9
 Sequence 9, Application US/08050132A
 Patient No. 5661007
 GENERAL INFORMATION:
 APPLICANT: Wozney, John M.
 TITLE OF INVENTION: BAP-9 COMPOSITIONS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: Legal Affairs - 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: US
 US-08-050-132A-9

RESULT 9
 Sequence 9, Application US/08050132A
 Patient No. 5661007
 GENERAL INFORMATION:
 APPLICANT: Wozney, John M.
 TITLE OF INVENTION: BAP-9 COMPOSITIONS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: Legal Affairs - 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: US
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,222A
 FILING DATE: 04-DEC-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/254,353
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kapinos, Ellen J.
 REGISTRATION NUMBER: 32,245
 REFERENCE/DOCKET NUMBER: GI 5186B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-1170
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-050-132A-9

Query Match 46.3%; Score 634; DB 1; Length 150;
 Best Local Similarity 92.7%; Pred. No. 4.5e-57;
 Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 135 YTAVGPPLARRKSTGASSHCQKTSRVNFEDIGWDSWITAPKDAYCKGGCFPLAD 194
 Db 28 HVAAGSTLARRKKSAGAGSHCQKTSRVNFEDIGWDSWITAPK 87

QY 195 DVTPPKTHAVQTLVHLKPPTKVKAACVPTKLSPLSILYKDM 254
 Db 88 DVTPPKTHAVQTLVHLKPPTKVKAACVPTKLSPLSILYKDM 147

QY 255 GCR 257
 Db 148 GCR 150

RESULT 10
 Sequence 9, Application US/08750222A
 Patient No. 6034061
 GENERAL INFORMATION:
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wozney, John M.
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Song, Jeffrey
 APPLICANT: Thies, Scott
 TITLE OF INVENTION: BAP-9 COMPOSITIONS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: Legal Affairs - 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: US
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,222A
 FILING DATE: 04-DEC-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/254,353
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kapinos, Ellen J.
 REGISTRATION NUMBER: 32,245
 REFERENCE/DOCKET NUMBER: GI 5186B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-1170
 TELEFAX: (617) 876-5851

CURRENT APPLICATION DATA:

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-750-222A-9

Query Match 46.3%; Score 634; DB 3; Length 150;
 Best Local Similarity 92.7%; Pred. No. 4.5e-57;
 Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 135 YTAGVPLLARKRKRTGASSHCOKSLRVNFEDIGWDSWILAPKEYEAYECKGGCFPLAD 194
 Db 28 HVAAGSTLARKRKRSAGSHCOKSLRVNFEDIGWDSWILAPKEYEAYECKGGCFPLAD 87
 Qy 195 DVTPTKHAIVOTLVHLKFPKVKRACCPYPTKLSPISTILYKDMGVPTLYHYEGMSVAC 254
 Db 88 DVTPTKHAIVOTLVHLKFPKVKRACCPYPTKLSPISTILYKDMGVPTLYHYEGMSVAC 147
 Qy 255 GCR 257
 Db 148 GCR 150

RESULT 11
 US-08-815-652B-9
 ; Sequence 9, Application US/08815652B
 ; Patent No. 6034062

GENERAL INFORMATION:
 APPLICANT: Wozney, John M.
 APPLICANT: Celeste, Anthony
 APPLICANT: Song, Jeffrey
 APPLICANT: Thies, R. Scott

TITLE OF INVENTION: BMP-9 COMPOSITIONS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: Legal Affairs - 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: US
 ZIP: 02140

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/254, 353A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kapinos, Ellen J.
 REGISTRATION NUMBER: 32,245
 REFERENCE/DOCKET NUMBER: GI 5186B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-1170
 TELEFAX: (617) 876-5951

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-815-652B-9

Query Match 46.3%; Score 634; DB 3; Length 150;
 Best Local Similarity 92.7%; Pred. No. 4.5e-57;
 Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 135 YTAGVPLLARKRKRTGASSHCOKSLRVNFEDIGWDSWILAPKEYEAYECKGGCFPLAD 194
 Qy 255 GCR 257
 Db 148 GCR 150

RESULT 12
 US-08-254-353A-9
 ; Sequence 9, Application US/08254353A
 ; Patent No. 6287816
 GENERAL INFORMATION:
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wozney, John M.
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Song, Jeffrey
 APPLICANT: Thies, Scott
 TITLE OF INVENTION: BMP-9 COMPOSITIONS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: Legal Affairs - 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: US
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/254, 353A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kapinos, Ellen J.
 REGISTRATION NUMBER: 32,245
 REFERENCE/DOCKET NUMBER: GI 5186B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 876-1170
 TELEFAX: (617) 876-5951

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-254-353A-9

Query Match 46.3%; Score 634; DB 4; Length 150;
 Best Local Similarity 92.7%; Pred. No. 4.5e-57;
 Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 135 YTAGVPLLARKRKRTGASSHCOKSLRVNFEDIGWDSWILAPKEYEAYECKGGCFPLAD 194
 Db 28 HVAAGSTLARKRKRSAGSHCOKSLRVNFEDIGWDSWILAPKEYEAYECKGGCFPLAD 87
 Qy 195 DVTPTKHAIVOTLVHLKFPKVKRACCPYPTKLSPISTILYKDMGVPTLYHYEGMSVAC 254
 Db 88 DVTPTKHAIVOTLVHLKFPKVKRACCPYPTKLSPISTILYKDMGVPTLYHYEGMSVAC 147
 Qy 255 GCR 257
 Db 148 GCR 150

RESULT 13
 PCP-US92-05374A-9

Sequence 9, Application PC/TUS9205374A
 GENERAL INFORMATION:

APPLICANT: Wozney, John M.

APPLICANT: Celeste, Anthony J.

TITLE OF INVENTION: BMP-9 COMPOSITIONS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

STREET: Legal Affairs - 87 CambridgePark Drive

CITY: Cambridge

STATE: MA

COUNTRY: US

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07084

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kapinos, Ellen J.

REGISTRATION NUMBER: 32,245

REFERENCE/DOCKET NUMBER: GI 5186C-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1210

TELEFAX: (617) 876-5851

TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT/US92-05374A-9

Query Match:

Score 634; DB 5; Length 150;

Best Local Similarity 92.7%; Pred. No. 4.5e-57;

Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 135 YTAGVPLARRKRGSTGASSHCOKTSLRVNFEDIGMDSWITAPKESDAYECKGGCFPLAD 194

Qy : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 28 HVAAGSTLARRKRSAGASHCOKTSLRVNFEDIGMDSWITAPKESDAYECKGGCFPLAD 87

Qy 195 DVTPRKHAIVQTVLHKEPTKVKGACCPVTKLSPISLYKDDMAGPYTLYHYGMSVAEC 254

Db 88 DVTPRKHAIVQTVLHKEPTKVKGACCPVTKLSPISLYKDDMAGPYTLYHYGMSVAEC 147

Qy 255 GCR 257

Db 148 GCR 150

RESULT 14
 PCT-US95-07084-9

GENERAL INFORMATION:

APPLICANT: Rosen, Vicki A.

APPLICANT: Wozney, John M.

APPLICANT: Celeste, Anthony J.

TITLE OF INVENTION: BMP-9 COMPOSITIONS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: Legal Affairs - 87 CambridgePark Drive

CITY: Cambridge

STATE: MA

COUNTRY: US

ZIP: 02140

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07084

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: LAZAR, STEVEN R.

REGISTRATION NUMBER: 32,618

REFERENCE/DOCKET NUMBER: GI 5206-CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 876-1170 x8260

TELEFAX: 617 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 312 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-247-908A-2

Query Match 38.0%; Score 519.5; DB 1; Length 312;
 Best Local Similarity 42.8%; Pred. No. 6.1e-45; Mismatches 73; Indels 43; Gaps 101; Matches 119; Conservative 43; MisMatches 73; Indels 43; Gaps 101;

Search completed: April 2, 2003, 14:53:07
Job time: 30 secs

Db	194 TDTITRLUDTRKLVDVRNSWESDVRSAVTKW--KNSPERNYGLEEVVSPKRG----- 245
Oy	70 SVPPESKMLPFFVYVFSNDSRSNGKETRDLIKEMIGHQEQMLVKAQYQAGESOEE 129
Db	246 -----A-ALSNHAVLRLRRESTDMD--DHAQHRRPLLTYD---DGKGSNSN 286
Oy	130 EGLDSYTAGVPLARRKRTGASSH-----COKTSLRNFEDIGWDSMIARKEYDA 181
Db	287 R-----VASHQKRANGKRKQRRLKANCRRSLSYVDFGWNWIVAPPGYDA 336
Oy	182 YECKGCCFFPLADDVTPTRKHAIVQTLVHLKFPKVGACCYPTKUSPISINKDDMGVPT 241
Db	337 YYCHGECPPFLADHNSTHAIWQTLVNSVNPPLAVPKACVPTDLSPISMYLNLNDQW 396
Oy	242 LKHYHVEGMSVAAECGCR 257
Db	397 LK-NYQDMVVEGCGCR 411
RESULT 2	
096504	PRELIMINARY; PRT; 361 AA.
ID	096504
AC	096504;
DT	01-MAY-1999 (TREMBREL 10, Created)
DT	01-MAY-1999 (TREMBREL 10, Last sequence update)
DE	Bone morphogenetic protein 2/4.
GN	AMPHIBMP2/4.
OS	Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OX	NCBI_TaxID=7739;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Medline-9940194; PubMed-9733108;
RA	Panopoulou G.D., Clark N.D., Holland N.D., Lehrach H., Holland N.D.;
RT	"AmphibMP2/4, a conserved bone morphogenetic protein closely related to Drosophila decapentaplegic and vertebrate BMP2 and BMP4: insights into evolution of dorsoventral axis specification.";
RT	Dev. Dyn. 213;130-139 (1998).
CC	-1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR	EMBL; AF068750; RAQ97488.1; -.
DR	HSSP; P12643; 3BMP.
DR	InterPro; IPR002405; Inhibin-alpha.
DR	InterPro; IPR001839; TGFb.
DR	InterPro; IPR001111; TGFb_N.
DR	ProDom; P000357; TGFb.
DR	SMART; SM00204; TGFb.
DR	PROSITE; PS00250; TGF_BETA_1.
DR	InterPro; IPR001111; TGFb_N.
DR	Pfam; PF00019; TGF-beta; 1.
DR	PRINTS; PR000659; INHIBINA.
DR	ProDom; P000357; TGFb.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1.
KW	glycoprotein.
SQ	SEQUENCE 405 AA; 45936 MW; D2EB2D2C7560ED13 CRC64;
Query Match 25.3%; Score 346; DB 5; Length 405; Best Local Similarity 31%; Pred. No. 2; 6-24; Indels 54; Gaps 6; Matches 76; Conservative 43; Mismatches 71; Indels 54; Gaps 6;	
Query Match 25.7%; Score 352; DB 5; Length 361; Best Local Similarity 35.3%; Pred. No. 6-24; Indels 48; Gaps 8; Matches 90; Conservative 31; Mismatches 86; Indels 48; Gaps 8;	
Oy	13 TGTKTPFLVSO--DIRDEGWETEVSSAVKVRARADSTNNKLNKEVTVQSHRECDTLI 69
Db	145 TDTITRLUDTRKLVDVRNSWESDVRSAVTKW--KNSPERNYGLEEVVSPKRG----- 196
Oy	70 SVPPESKMLPFFVYVFSNDSRSNGKETRDLIKEMIGHQEQMLVKAQYQAGESOEE 129
Db	197 -----ALSNHIVYLRLRSTMD--DHSWQHRRPLLTYD---DGKGSNSN 237
Oy	130 EGLDSYTAGVPLARRKRTGASSH-----COKTSLRNFEDIGWDSMIARKEYDA 193
Db	238 R-----VASHQKRANGKRKQRRLKANCRRSLSYVDFGWNWIVAPPGYDA 287
Oy	183 ECKGCCFFPLADDVTPTRKHAIVQTLVHLKFPKVGACCYPTKUSPISILYKODMGVPTL 242
RESULT 3	
09588	PRELIMINARY; PRT; 405 AA.
ID	09588
AC	09588;
DT	01-MAY-2000 (TREMBREL 13, Created)
DT	01-MAY-2000 (TREMBREL 13, Last sequence update)
DT	01-JUN-2002 (TREMBREL 21, Last annotation update)
DE	PP-BMP2/4.
GN	PP-BMP2/4.
OS	Psychodera flava.
OC	Eukaryota; Metazoa; Hemichordata; Enteropneusta; Psychoderidae;
OX	NCBI_TaxID=63121;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Harada Y.;
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Okai N., Taguchi S., Tagawa K., Satoh N.;
RT	"Developmental expression of hemichordate orthologs of BMP-4, otx and dlx: insights into deuterostome archetype and evolution of chordate body plan.";
RT	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL	-1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR	EMBL; AB028219; BA89012.1; -.
DR	HSSP; P12643; 3BMP.
DR	InterPro; IPR002405; Inhibin_alpha.
DR	InterPro; IPR001839; TGFb.
DR	InterPro; IPR001111; TGFb_N.
DR	Pfam; PF00019; TGF-beta; 1.
DR	PRINTS; PR000659; INHIBINA.
DR	ProDom; P000357; TGFb.
DR	SMART; SM00204; TGFb.
DR	PROSITE; PS00250; TGF_BETA_1.
KW	glycoprotein.
SQ	SEQUENCE 405 AA; 45936 MW; D2EB2D2C7560ED13 CRC64;
Query Match 25.3%; Score 346; DB 5; Length 405; Best Local Similarity 31%; Pred. No. 2; 6-24; Indels 54; Gaps 6; Matches 76; Conservative 43; Mismatches 71; Indels 54; Gaps 6;	
Oy	23 DIRDEGWETEVSSAVKVRARADSTNNKLNKEVTVQSHRECDTLI-----VOSHRESC---DTPLDISVPP 73
Db	207 DIRDEGWETEVSSAVKVRARADSTNNKLNKEVTVQSHRECDTLI-----VOSHRESC---DTPLDISVPP 73
Oy	74 GSKNLPFFVYVFSNDSRSNGKETRDLIKEMIGHQEQMLVKAQYQAGESOEEGLD 133
Db	267 WQORPLLTYD---SKRPT-----SKRNS-----SKRNS-----SKRNS----- 291
Oy	134 GTYAVPLARRKRTGASSHCKTSLRNEDIGWDSMIARKEYDAECKGCCFRLA 193
Db	292 -----ERKGGRKLPKNCRRLSVDGFDVGNHDTWAPPGKNAFYCDGCPFPLA 342
Oy	194 DDTPTKHAIVQTLVHLKFPKVGACCYPTKUSPISILYKODMGVPTLHYGMSVAE 253
Db	343 DHLNSTHAIWQTLVHLKFPKVGACCYPTKUSPISILYKODMGVPTLHYGMSVAE 401
Oy	254 CGCR 257
Db	402 CGCR 405
RESULT 4	

SQ	SEQUENCE	614 AA;	69055 MW;	DOF20M4093403DCF	CRC64;	Db	20	DTSSATWDVFDVGPIKPLQHRTAEDTRILCLSLISAVS---DSNEAVHPGMLGLS	74	
Query	Match	24.3%;	Score	333;	DB 5;	Length	614;	Query	79 -----PFFVFSNDRNGTKETRDLKEMI-----GHEQTPM 111	
Best	Local	Similarity	33.3%;	Pred.	No. 7,	9e-23;	Matches	84;	REDDOTHERALYAFSQAR---RKENIFREIREEKIRAMSKRSKFSNPTPEHSIKHPRHR 131	
Matches	84;	Conservative	37;	Mismatches	87;	Indels	44;	Oy	19 LVSDDIRDGWET--LEYSAYKVRWRASSTNNKLNKLETVOSR 61	
Db	394	LDTKTVRLNSTETVSLDVQPAVDRWL--ATPOKNYGLVEVRTNRSKLPAPHVHVRLLR	450	Oy	112 LVTKTKNAYQGAESQESEGCGYTAGPLARRKRTGASSHIIOKTSARVNEDIGDS 65					
Oy	66	TLDTSVPPESKNLPEVVFVFSNDRNGTKETRDLKEMI-----GHEQTPM	125	Oy	172 WIAPKEYAECKGGCFPLADDNVPKTHAVQTVLHKEPTKVGACCVPMKLSPI 231					
Db	451	SADEAHEDWQHKQPLFLFTYDD--GRHRSR--STRDVSGRE-----GGGGGGGR	496	Oy	177 WIAPLDYEAHCGLCDFPLRSRHLPEPTNHAITQTLMSMDPESTPPSCCVPSKLSPI 236					
Oy	126	SQEERGLDGTAVQPLARRKRTGASSHIIOKTSARVNEDIGDSWITAPKEDEVCK	185	Oy	232 LYKDDMGVTLKIHIEGSAECCR 257					
Db	497	NRRHQ-----RSRKKNNNDNCRHSLTVDFODGNSDWIVAPPGYDAYYCH	543	Db	237 LYIDS-GNNVYKQYEDAVVYESGCR 261					
Oy	186	GGCFFPLADDVTPKTHAVQTVLHKEPTKVGACCVPMKLSPI 245	Oy	308 QBUVQB ID QBUVQB PRELIMINARY; PRT; 391 AA.						
Db	544	GKCCDPLADHNSPNHAWQTLVNLNPKGKPAACVPTQLEGISMLYLNQDRIVWLK-N	602	Result	8	QBUVQB ID QBUVQB PRELIMINARY; PRT; 391 AA.				
Oy	246	YEGMVAECCR 257	Oy	309 QBUVQB ID QBUVQB PRELIMINARY; PRT; 391 AA.						
Db	603	YQDMKTVVGCCR 614	Db	310 QBUVQB ID QBUVQB PRELIMINARY; PRT; 391 AA.						
RESULT 7										
09W6CO	SEQUENCE	99 AA;	PRELIMINARY;	PRT;	261 AA.	AC	QBUVQB;	OBUVQB;	OBUVQB;	
ID	09W6CO	OY	01-NOV-1999 (Tremblrel. 12, Created)	DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)	DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)	DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)	
AC	09W6CO	DT	01-NOV-1999 (Tremblrel. 12, Last sequence update)	DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)	DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)	DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)	
AC	09W6CO	DE	Growth/differentiation factor 7 (Fragment).	DE	Anti-dorsalizing morphogenetic protein.	OS	Brachydanio rerio (Zebrafish) (Zebrafish) (Zebrafish)	OS	Brachydanio rerio (Zebrafish) (Zebrafish) (Zebrafish)	
GN	GN	GN	Brachydanio rerio (Zebrafish) (Zebrafish) (Zebrafish)	GN	Brachydanio rerio (Zebrafish) (Zebrafish) (Zebrafish)	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OS	OS	OS	Brachydanio rerio (Zebrafish) (Zebrafish) (Zebrafish)	OS	Brachydanio rerio (Zebrafish) (Zebrafish) (Zebrafish)	OC	Actinopterygii; Neopterygii; Cypriniformes;	OC	Actinopterygii; Neopterygii; Cypriniformes;	
OC	OC	OC	Actinopterygii; Neopterygii; Cypriniformes;	OC	Actinopterygii; Neopterygii; Cyprinidae; Danio.	OC	Actinopterygii; Neopterygii; Cyprinidae; Danio.	OC	Actinopterygii; Neopterygii; Cyprinidae; Danio.	
OC	OC	OC	Actinopterygii; Neopterygii; Cyprinidae; Danio.	OC	NCBI_TAXID=7955;	RN	[1]	RN	[1]	
OX	OX	OX	NCBI_TAXID=7955;	OX	SEQUENCE FROM N.A.	RP	MEDLINE-21614594; MEDLINE-11748836;	RP	MEDLINE-21614594; MEDLINE-11748836;	
RN	RN	RN	Lele Z., Nowak M., Hammerschmidt M.;	RN	Lele Z., Nowak M., Hammerschmidt M.;	RA	Zebrachish admin is required to restrict the size of the organizer and	RA	Zebrachish admin is required to restrict the size of the organizer and	
RX	RX	RX	to promote posterior and ventral development.;	RX	to promote posterior and ventral development.;	RX	to promote posterior and ventral development.;	RX	to promote posterior and ventral development.;	
RA	RA	RA	Dev. Dyn. 222:681-687 (2001);	RA	Dev. Dyn. 222:681-687 (2001);	RA	EMBL: AF418561; AR495021; -.	RA	EMBL: AF418561; AR495021; -.	
RA	RA	RA	EMBL: AF418561; AR495021; -.	RA	EMBL: AF418561; AR495021; -.	DR	Interpro; IPRO01833; TGFb.	DR	Interpro; IPRO01833; TGFb.	
RA	RA	RA	Interpro; IPRO01111; TGFb_N.	DR	Interpro; IPRO01111; TGFb_N.	DR	Pfam; PF00019; TGF-beta; 1.	DR	Pfam; PF00019; TGF-beta; 1.	
RA	RA	RA	Pfam; PF00688; TGFb_propeptide; 1.	DR	Pfam; PF00688; TGFb_propeptide; 1.	DR	PRODom; P0000357; TGFb; 1.	DR	PRODom; P0000357; TGFb; 1.	
RA	RA	RA	SMART; SM0204; TGFb; 1.	DR	SMART; SM0204; TGFb; 1.	DR	PROSITE; PS00250; TGF_beta_1; UNKNOWN_1.	DR	PROSITE; PS00250; TGF_beta_1; UNKNOWN_1.	
RA	RA	RA	SEQUENCE	SO	SEQUENCE	391 AA;	43792 MW;	F89885D22364962B	CRC64;	
RT	RT	RT	Query	Oy	5 DSETWDQAGTKTLVLSQ---DIRDEGNETLEYSAYKVRWRASSTNNKLNKLETVOSR	61	Query	5 DSETWDQAGTKTLVLSQ---DIRDEGNETLEYSAYKVRWRASSTNNKLNKLETVOSR	61	
RT	RT	RT	Match	Oy	154 DSKKNVSGOKK---LSSRLRVLPHSGWEVTITQAVSRM-SDEGSNLLG-LVSURL 209	61	Match	154 DSKKNVSGOKK---LSSRLRVLPHSGWEVTITQAVSRM-SDEGSNLLG-LVSURL 209	61	
RT	RT	RT	Best	Oy	62 ESDTLDISVPPGSKKNLPEVVFVFSNDRNGTKETRDLKEMI-----GASHIQKTSLRVNEDIGW	121	Local	Oy	62 ESDTLDISVPPGSKKNLPEVVFVFSNDRNGTKETRDLKEMI-----GASHIQKTSLRVNEDIGW	121
RT	RT	RT	Similarity	Oy	210 GS---QMDLM-----VPERASGDH-----RHSKQPMVLTIDRR 243	121	Similarity	Oy	210 GS---QMDLM-----VPERASGDH-----RHSKQPMVLTIDRR 243	121
RT	RT	RT	Score	Oy	122 GAGESQEEGLD---GTTAVGFLKARRKST-----GASHIQKTSLRVNEDIGW	169	Score	Oy	122 GAGESQEEGLD---GTTAVGFLKARRKST-----GASHIQKTSLRVNEDIGW	169
RT	RT	RT	32.3%;	Oy	244 ANSLATSKGSDPSGGQASQPLSPVSPASRRSSRSVYDERGEKMACQQRPLVYFEICW	303	32.3%;	Oy	244 ANSLATSKGSDPSGGQASQPLSPVSPASRRSSRSVYDERGEKMACQQRPLVYFEICW	303
RT	RT	RT	Pred.	Oy	170 DSWLAPKEDEVCKGGCFPLADDVPTKIAVOTLVH-LKFPTKVGKACCPKLSPI 228	303	No. 1.7e-22;	Oy	170 DSWLAPKEDEVCKGGCFPLADDVPTKIAVOTLVH-LKFPTKVGKACCPKLSPI 228	303
RT	RT	RT	No. 1.7e-22;	Oy	304 SGWIVSPKGKYNACKGKSCIFPLSNSRNPHTNHAIWOSINTLKNKGQIOTPCCVFDKLYS	363	Mismatches	Oy	304 SGWIVSPKGKYNACKGKSCIFPLSNSRNPHTNHAIWOSINTLKNKGQIOTPCCVFDKLYS	363
RT	RT	RT	95;	Oy	229 ISILYKDDMGVPTKHYEGMSVACCCR 257	363	Indels	Oy	229 ISILYKDDMGVPTKHYEGMSVACCCR 257	363
RT	RT	RT	7;	Oy	364 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Gaps	Oy	364 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	7;	Oy	305 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	305 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	261;	Oy	306 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	306 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	24.1%;	Oy	307 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 13;	Oy	307 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	Length	Oy	308 ISLXFDDEENVK-QDDDMAGSCGR 391	363	61;	Oy	308 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	Score	Oy	309 ISLXFDDEENVK-QDDDMAGSCGR 391	363	329.5;	Oy	309 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	310 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	310 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	Length	Oy	311 ISLXFDDEENVK-QDDDMAGSCGR 391	363	61;	Oy	311 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	312 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	312 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	313 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	313 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	314 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	314 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	315 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	315 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	316 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	316 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	317 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	317 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	318 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	318 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	319 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	319 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	320 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	320 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	321 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	321 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	322 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	322 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	323 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	323 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	324 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	324 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	325 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	325 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	326 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	326 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	327 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	327 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	328 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	328 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	329 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	329 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	330 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	330 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	331 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	331 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	332 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	332 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	333 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	333 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	334 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	334 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	335 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	335 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	336 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	336 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	337 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	337 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	338 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	338 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	339 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	339 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	340 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	340 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	341 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	341 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	342 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	342 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	343 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	343 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	344 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	344 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	345 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	345 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	346 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	346 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	347 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	347 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	348 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	348 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	349 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	349 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	350 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	350 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	351 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	351 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	352 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	352 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	353 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	353 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	354 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	354 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	355 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	355 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	356 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	356 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	357 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Length	Oy	357 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	358 ISLXFDDEENVK-QDDDMAGSCGR 391	363	Score	Oy	358 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;	Oy	359 ISLXFDDEENVK-QDDDMAGSCGR 391	363	DB 5;	Oy	359 ISLXFDDEENVK-QDDDMAGSCGR 391	363
RT	RT	RT	DB 5;</							

RESULT 9		RA Smith J.C.;	
ID 073818	PRELIMINARY;	PRY;	400 AA.
ID 073818;			
AC 073818;			
DT 01-AUG-1998 (TREMBLrel. 07, Created)			
DT 01-AUG-1998 (TREMBLrel. 01, Last sequence update)			
DE protein 4.			
GN BMP-4.			
OS Xenopus laevis (African clawed frog)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
Xenopodinae; Xenopus.			
NCBI_TAXID=8355;			
RN [1]			
RP SEQUENCE FROM N.A.			
RP SEQUENCE FROM N.A.			
RA Smith J.C.;			
RL Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.			
RN [2]			
RP SEQUENCE OF 1-20 FROM N.A.			
RA Smith J.C.;			
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.			
RA Dale L.; Howes G.; Price B.M.; Smith J.C.;			
RT "Bone morphogenetic protein 4: a ventralizing factor in early Xenopus development. #"			
RT Development 115:573-585(1992).			
RL [3]			
RN SEQUENCE FROM N.A.			
RA Met A.; Knoechel S.; Buechler P.; Koester M.; Knoechel W.;			
RA Kim J.; Ault K.T.; Chen H.D.; Xu R.H.; Roh D.H.; Lin M.C.; Park M.J.;			
RA Kung H.F.;			
RT "Transcriptional regulation of BMP-4 in the Xenopus embryo: analysis of genomic BMP-4 and its promoter.";			
RT Biophys. Res. Commun. 250:516-520(1998).			
RL 1-SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
CC EMBL; AF05764; AAC61694; 1; -.			
DR HSSP; P12643; 3BMP.			
DR Interpro; IPR00839; TGFb.			
DR Interpro; IPR00111; TGFb_N.			
DR Pfam; PF00019; TGF-beta_1.			
DR Pfam; PF00688; TGFb_propeptide; 1.			
DR SMART; SM00204; TGFb; 1.			
DR PROSITE; PS00250; TGF_BETA_1; 1.			
DR Glycoprotein.			
KW SEQUENCE 400 AA; 45810 MW; A3147B4FACB4553F CRC64;			
Query Match 23.9%; Score 326.5; DB 13; Length 400; Best Local Similarity 32.8%; Pred. No. 1.8e-22; Matches 78; Conservative 35; Mismatches 72; Indels 53; Gaps 7;			
QY 29 WETLEYSSAVKRWRADSTINKKLEV---TVQSHRESCDLIDSIVPP---GSKNLP 79			
DB 207 WESFDVSPALMRWTRDKQINHGKLNQTKTHQKRISRLSILPQEDAWSQMRP 266			
QY 80 FFWVVSNDRNGTKTRDILKEMIGHQETMLVKTAKNAYOGAGESQEEFGDQTYAVG 139			
DB 267 LLITPSHGR-----GH---ALTRRSRS----- 287			
QY 140 PLARKRKGASSHQKSLRVNFEDIGWDSMILAKPKEYDVEKGCFPLADYTP 199			
DB 288 ---PKQQRPKRNKHNRLQYVDFSDVGMWNIWAPPGQAFYCHGDCPFPLADHINST 344			
QY 200 KHAIVOTLVHKFPKVKGACCVPKLSFISILYKDDMGVPLVKHYEGSVAEGCR 257			
DB 345 NHAIVOTLVN-SVNASIPKACCVPTELSAISMLYLDYDKVVLK-NYQEMVVEGCR 400			
RESULT 10	RESULT 11		
ID 091703	PRELIMINARY;	PRY;	400 AA.
ID 091703;			
AC 091703; 01-Nov-1996 (TREMBLrel. 01, Created)			
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DE protein 4.			
GN BMP-4.			
OS Xenopus laevis (African clawed frog)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.			
NCBI_TAXID=8355;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Shih T.-J.; Chen C.-P.; Hwang S.-P.-L.;			
RT "Uniform distribution of Sea Star BMP-2/4 mRNA in Embryos at the Later Stages of Embryonic Development.";			
RT Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.			
RL EMBL; AF347388; AAU73188; 1; -.			
DR Interpro; IPR001839; TGFb.			
DR Interpro; IPR00111; TGFb_N.			
DR Pfam; PF00019; TGF-beta_1.			
DR Pfam; PF00688; TGFb_propeptide; 1.			
DR PROSITE; PS00204; TGFb; 1.			
DR SMART; SM00250; TGF_BETA_1; 1.			
RP SEQUENCE FROM N.A.			

Db 264 PLPSVPASRRSPRSVYDERGEKMACQROPLVDFERIGWSGWIYSPKGYNAYHCKGSCI 323
Qy 190 FPLADDPVTPKHAIVOTLVH-LKPTKGACVPTLSP'SILKDDMCGVPTKHYHG 248
Db 324 FPLSOMRPTNHAIVOSINTLKLNGIOTPCCVPDKLYSISLUFDDENVVLIK-QYDD 382
Qy 249 MSVAREGCR 257
Db 383 MVAGSCGCR 391

search completed: April 2, 2003, 14:51:41
Job time : 88 secs

Copyright (C) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.4-p5-4578			
OM protein - protein search, using sw model				
Run on:	April 2, 2003, 14:40:40 ; Search time 26 Seconds			
	{without alignments} 409,978 Million cell updates/sec			
Title:	US-10-002-278-9			
Perfect score:	1368			
Sequence:	1 DVLEDSEFWDQATGKTFLV..... .CVPTLKYHVEGMSVAECGCR 257			
Scoring table:	BLOSUM62			
Database :	Swissprot_40:*			
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	1349.5	98.6	428	1 GDF2_MOUSE
2	1146.5	83.8	429	1 GDF2_HUMAN
3	808.5	59.1	427	1 DS1L_CHICK
4	516.5	37.8	424	1 BM10_RUMAN
5	507	37.1	420	1 BM10_MOUSE
6	345	25.2	408	1 BMP4_HUMAN
7	342.5	25.0	408	1 BMP4_RAT
8	341	24.9	408	1 BMP4_DAMDA
9	337.5	24.7	408	1 BMP4_MOUSE
10	336	24.6	409	1 BMP4_RABIT
11	330	24.1	436	1 GDF6_BOVIN
12	327.5	23.9	405	1 BMP4_CHICK
13	325	23.8	1 DECA_DROME	Zimars, T.A., Koniaris, L.G., Sitzmann, J.V., Lee, S.-J.; "Growth/differentiation factor-2, a new TGF-beta family member with bone promoting activities"; submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
14	324.5	23.7	621	1 DECA_DROPS
15	323	23.6	593	1 DECA_DROSOPHILA
16	319	23.3	398	1 BMPB_XENLA
17	316.5	23.1	401	1 BMP4_XENLA
18	316	23.1	395	1 BMP2_RABIT
19	315	23.0	1 BMP2_XENLA	
20	314.5	23.0	430	1 BMP7_MOUSE
21	314	23.0	393	1 BMP2_RAT
22	313	22.9	394	1 BMP2_MOUSE
23	312.5	22.8	454	1 BMP5_HUMAN
24	312	22.8	125	1 GDF6_MOUSE
25	311	22.7	396	1 BMP2_HUMAN
26	311	22.7	399	1 BMP2_MOUSE
27	310.5	22.7	461	1 BMP1_STRP6
28	310	22.7	396	1 BMP2_DAMDA
29	312.5	22.4	353	1 BMP2_CHICK
30	307	22.4	501	1 GDF5_HUMAN
31	305.5	22.3	431	1 BMP7_HUMAN
32	305.5	22.3	452	1 BMP5_MOUSE
33	305.5	22.3	495	1 GDF5_MOUSE

RT differentiation by dorsalin-1, a novel tcf beta family member.";
 RL Cell 73:687-702(1993).
 CC -!- FUNCTION: APPEARS TO REGULATE CELL DIFFERENTIATION WITHIN THE
 NEURAL TUBE. MAY REGULATE THE DIFFERENTIATION OF CELL TYPES ALONG
 THE DORSOVENTRAL AXIS OF THE NEURAL TUBE, ACTING IN CONJUNCTION
 WITH DISTINCT VENTRALIZING SIGNALS FROM THE NOTOCHORD AND FLOOR
 PLATE. CONTROLS THE CELL DIFFERENTIATION IN THE NEURAL TUBE IN
 SEVERAL WAYS: (1) PROMOTES THE DIFFERENTIATION OF CELL TYPES THAT
 DERIVE FROM THE DORSAL NEURAL TUBE. (2) ENSURES THAT THE DORSAL
 NEURAL TUBE IS REFRACOTORY TO VENTRALIZING SIGNALS FROM THE
 NOTOCHORD. (3) CAN DIFFUSE AND INFLUENCE THE FATE OF CELLS IN MORE
 VENTRAL REGIONS OF THE NEURAL TUBE.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED SELECTIVELY IN THE DORSAL NEURAL
 TUBE. LOWER LEVELS SEEN IN KIDNEY AND MYOMALIC CELLS.
 CC -!- DEVELOPMENTAL STAGE: IS NOT EXPRESSED IN NEURAL CELLS AT STAGES
 BEFORE NEURAL TUBE CLOSURE. IS EXPRESSED AT HIGH LEVELS IN THE
 DORSAL THIRD OF THE NEURAL TUBE, BEGINNING AT THE TIME OF NEURAL
 TUBE CLOSURE, BUT NOT BY VENTRAL NEURAL CELLS OR BY NONNEURAL
 CELLS. DORSAL RESTRICTION PERSISTS IN THE SPINAL CORD AT STAGES
 AFTER THE ONSET OF NEURONAL DIFFERENTIATION. AT LATER STAGES OF
 SPINAL DEVELOPMENT, IS RESTRICTED TO THE DORSOMEDIAL REGION OF
 THE SPINAL CORD, INCLUDING BUT NOT CONFINED TO THE ROOF PLATE.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL: L12032; RAA8752.1; -.
 CC DR PRODom: PD000357; TGFb; 1.
 CC DR SMART: SM0204; TGF_BETA_1; 1.
 CC DR PROSITE: PS00250; TGF_BETA_1; 1.
 CC KW SIGNAL; Growth factor; Cytokine; Glycoprotein.
 CC FT SIGNAL 1 20 POTENTIAL.
 CC FT PROPEP 21 318
 CC FT CHAIN 319 427 DORSALIN-1.
 CC FT DISULFID 325 391 BY SIMILARITY.
 CC FT DISULFID 354 424 BY SIMILARITY.
 CC FT DISULFID 358 426 BY SIMILARITY.
 CC FT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SO SEQUENCE 427 AA; 48626 MW; 23AA42DC7085FABC CRC64;
 CC Query Match 59.1%; Score 808.5; DB 1; Length 427;
 CC Best Local Similarity 61.9%; Pred. No. 1.5e-64;
 CC Matches 161; Conservative 31; Mismatches 59; Indels 9; Gaps 5;
 CC SEQUENCE FROM N.A.
 CC Celeste A.J.;
 CC RA Homo sapiens bone morphogenetic protein 10 (BMP-10) mRNA.;"
 CC DR Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL: AF101441; AAC77462.1; -.
 CC DR HSSP; P12643; 3BMP.
 CC DR InterPro: IPR002405; Inhibin_alpha.
 CC DR InterPro: IPR001839; TGFb.
 CC DR InterPro: IPR00111; TGFb_N.
 CC DR Pfam: PF00019; TGF-beta_1.
 CC DR Pfam: PF00688; TGFb_propeptide; 1.
 CC DR PRINTS; PRO0659; INHIBINA.
 CC DR PRODom: PD000357; TGFb; 1.
 CC DR PROSITE: PS00250; TGF_BETA_1; 1.
 CC KW SIGNAL; Growth factor; Cytokine; Glycoprotein.
 CC FT SIGNAL 1 21 POTENTIAL.
 CC FT PROPEP 22 316
 CC FT CHAIN 317 424 BONE MORPHOGENETIC PROTEIN 10.
 CC FT DISULFID 323 389 BY SIMILARITY.
 CC FT DISULFID 352 421 BY SIMILARITY.
 CC FT DISULFID 356 423 BY SIMILARITY.
 CC FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 424 AA; 48047 MW; 3FDB3H7221BB2254 CRC64;

Qy 1 DYLEDSEETWDQATGKTFLVSQIRDSEGWTLEYSSAVKVRWADSTNNKLEVTVQH 60
 Db 174 DYL-DDGHWENKESTKSLVLSIQDCQWEMFREVSSAVKVRWADSTNNKLEVTVQH 232
 Qy 61 RES--CDQDLSVPGSKNLPLPFVWSNDRSGTKETRDILKEMIGHQROETMLVKTAK 117
 Db 233 DLSGFPCKGKLDITVTHDKTNPPLIVSNDRSGTKEV-LREMTVHQESYLNKLK 291
 Qy 118 NAVGAGESEEEGLDTAVGLLARSTGASSHCKTSRSLRNEDIGWDSMIAPK 177
 Db 292 NDSSSEEERGEEKAI--ARPROHRSRSRKSRSIGA-NHCRRTSLHVNEKEIGWDSMIAPK 347

RESULT 4

DB	QY	DR	QY	DR
348	178	348	178	348
DYEAFFCKGGCFPLDNVTPTKHAIVOTLVHKLKPTKVGKACCVPTKLSPISTLYKDD	EYDAVECKGGCFPLADVTPTKHAIVOTLVHKLKPTKVGKACCVPTKLSPISTLYKDD	DYEAFFCKGGCFPLDNVTPTKHAIVOTLVHKLKPTKVGKACCVPTKLSPISTLYKDD	EYDAVECKGGCFPLADVTPTKHAIVOTLVHKLKPTKVGKACCVPTKLSPISTLYKDD	DYEAFFCKGGCFPLDNVTPTKHAIVOTLVHKLKPTKVGKACCVPTKLSPISTLYKDD
408	238	408	238	408
GYPTLKVHFGMSYAECCR	GYPTLKVHFGMSYAECCR	GYPTLKVHFGMSYAECCR	GYPTLKVHFGMSYAECCR	GYPTLKVHFGMSYAECCR
427	257	427	257	427
QPTLIVNYGGKVACGCR	QPTLIVNYGGKVACGCR	QPTLIVNYGGKVACGCR	QPTLIVNYGGKVACGCR	QPTLIVNYGGKVACGCR

Qy 59 S-HRESCDT--LDSVPGSKNLPLPFVWSNDRSGTKETRDILKEMIGHQROETMLVKTAK 113
 Qy 1 DYLEDSEETWDQATGKTFLVSQIRDSEGWTLEYSSAVKVRWADSTNNKLEVTVQH 58
 Db 169 EYLE SKGDNIEGRMLVLYVSEGEYIGCNSWEMTFDVAIRWQSGST--HOLEVHIE 225

RT Cloning and sequence of bone morphogenetic protein 4 (BMP-4) from a
 RT human placental cDNA library. ";

RL DNA Seq. 5:273-275 (1995).

CC MESODERM INDUCTION, CARTILAGE AND BONE FORMATION. ALSO ACT IN
 REPAIR.

CC SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.

CC TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LOWER LEVELS SEEN
 IN THE KIDNEY, PRESENT ALSO IN NORMAL AND NEOPLASTIC PROSTATE
 TISSUES, AND PROSTATE CANCER CELL LINES.

CC !-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 or send an email to license@isb-sib.ch).

DR EMBL: M22490; AAA51835.1; -.

DR EMBL: D020546; AABH20546.1; -.

DR EMBL: D30751; BAAH6410.1; -.

DR PIR: C3728; C3728.

DR HSSP: P12643; 3BMP.

DR Gene: IRNC:1071; BMP4.

DR MIM: 112262; -.

DR InterPro: IPR001839; TGFB.

DR InterPro: IPR01111; TGFB_N.

DR Pfam: PF00019; TGF-beta; 1.

DR Prodom: PD000357; TGFB; 1.

DR SMART: SM00204; TGFB; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

DR SIGNAL: 1 19 POTENTIAL.

FT PROPEP 20 292 BONE MORPHOGENETIC PROTEIN 4.

FT CHAIN 293 408 BY SIMILARITY.

FT DISULFID 308 373 BY SIMILARITY.

FT DISULFID 337 405 BY SIMILARITY.

FT DISULFID 341 407 BY SIMILARITY.

FT DISULFID 372 372 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 208 208 N LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 365 365 V -> A (IN REF. 2 AND 3).

SO SEQUENCE 408 AA: 465555 MW; 79B01179DBB96204 CRC64;

Query Match 25.2%; Score 345; DB 1; Length 408;
 Best Local Similarity 35.9%; Pred. No. 2.7e-23; Matches 85; Conservative 28; Mismatches 76; Indels 48; Gaps 7;

Qy 29 WETLIVSSAVKRVRASTDSTNNKLETV---VOSHRECDTLISVPGSKN---LPP 80

Db 212 WETFDVSPAVLWRTREREKOPNYGLAIEVTHLHOTRTHQHVRISRLSPQSGNNAQLRPL 271

Qy 81 FWVTSNDRNGTKTETRDLKEMIGHQETMVKTKNAYQAGAESQEEEGLOGYTAQGP 140

Db 272 LVTFGHD-GRGHALTTRRRAKSPKHSQR----- 300

Qy 141 LLARKRSTGASSHQKTSLRNFEDIGWDSWIAKPKEYDVECKGGCFPLADDVPTK 200

Db 301 --ARK---NPKCRRLSLYFEDSGWNWIVAPGQOAFYCHGDCFPPLADHLNSTN 353

201 HATVOTVHLKFPKVGACCPFTKUSLPIKDDGMVPTLKKXHVEGMSVAEGCR 257

354 HATVOTLVN-SVNSIIPRACVYPTELSAISMLYDVEYDKVULK-NYQEWVEGGCR 408

BMP4_RAT ID BMP4_RAT STANDARD; PRT; 408 AA.

AC 0068376; DT 01-JUN-1994 (Rel. 29, Created)
 CC 01-JUN-1994 (Rel. 29, last sequence update)

DR 16-OCT-2001 (Rel. 40, last annotation update)

DE Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B).

GN BMP4 OR BMP-4 OR DVR-4

OS Rattus norvegicus (Rat).

CC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 NCBI_TaxID=10116; NCBI_TaxID=10116;

[1] RP SEQUENCE FROM N.A.

RX MEDLINE-93385158; Pubmed=8373807;

RA Chen D, Feng J Q, Feng M, Harris M A, Mundy G R, Harris S E;

RR rat calvarial cell.;

RL Bioclim. Biophys. Acta 1174:289-292 (1993).

CC !-! FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.

CC !-! SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC !-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL: 222607; CAA0329.1; -.

DR PIR: S33173; S33173.

DR SMART: S38343; S38343.

DR HSSP: P12643; 3BMP.

DR InterPro: IPR001839; TGFB.

DR InterPro: IPR01111; TGFB_N.

DR Pfam: PF00019; TGF-beta; 1.

DR Prodom: PD000357; TGFB; 1.

DR SMART: SM00204; TGFB; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

DR SIGNAL: 1 19 POTENTIAL.

FT PROPEP 20 292 BONE MORPHOGENETIC PROTEIN 4.

FT CHAIN 293 408 BY SIMILARITY.

FT DISULFID 308 373 BY SIMILARITY.

FT DISULFID 337 405 BY SIMILARITY.

FT DISULFID 341 407 BY SIMILARITY.

FT DISULFID 372 372 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 209 209 N LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 408 AA: 465440 MW; 61E92B4B8D5624F3 CRC64;

Query Match 25.0%; Score 342.5; DB 1; Length 408;
 Best Local Similarity 35.4%; Pred. No. 4.5e-23; Matches 84; Conservative 31; Mismatches 73; Indels 49; Gaps 7;

Qy 29 WETLIVSSAVKRVRASTDSTNNKLETV---VOSHRECDTLISVPGSKN---LPP 80

Db 213 WETFDVSPAVLWRTREREKOPNYGLAIEVTHLHOTRTHQHVRISRLSPQSGNNAQLRPL 272

Qy 81 FWVTSNDRNGTKTETRDLKEMIGHQETMVKTKNAYQAGAESQEEEGLOGYTAQGP 140

Db 273 LVTFGHDGDR-----GH---TIRRRAKSPK----- 295

Qy 141 LLARKRSTGASSHQKTSLRNFEDIGWDSWIAKPKEYDVECKGGCFPLADDVPTK 200

Db 296 -HFFQSRKRNKCRRLSLYFEDSGWNWIVAPGQOAFYCHGDCFPPLADHLNSTN 353

RESULT 7

Db 350 NHAVQTLVN-SVNSSIPKACCPVPTLSATSMYLDEYDKVWLK-NYQEMVYEGCGCR 405 PROSITE; PS00250; TGF-BETA_1; 1. DR
ID DECA_DROME STANDARD PRT; 568 AA. KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
Signal.

RESULT 13 FT PROPER 1 15 PROSITE; PS00250; TGF-BETA_1; 1.
ID DECA_DROME STANDARD PRT; 568 AA. FT PROPER 1 15 PROSITE; PS00250; TGF-BETA_1; 1.
AC P07713; P91651; FT CHAIN 457 588 PROPER; DRCAPIENTAPLEGIC PROTEIN.
DT 01-APR-1998 (Rel. 07, Created) FT DISUFLID 487 553 BY SIMILARITY.
DT 01-APR-1998 (Rel. 07, Last sequence update) FT DISUFLID 516 585 BY SIMILARITY.
DT 15-DEC-1998 (Rel. 37, Last annotation update) FT DISUFLID 520 587 BY SIMILARITY.
DE Decapentaplegic protein precursor (DPP-C protein). FT DISUFLID 552 592 INTERCHAIN (BY SIMILARITY).
GN DPP. FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
OS Drosophila melanogaster (Fruit fly). FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; FT CARBOHYD 377 377 N-LINKED (GLCNAC. . .) (POTENTIAL).
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; FT VARIANT 529 529 V->M (IN STRAIN DP CN BW).
OC Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila. FT VARIANT 559 559 K->G (IN STRAIN DP CN BW).
OC NCBI_TaxID=7277; FT VARIANT 121 121 HA->QP (IN STRAIN DP CN BW).
RN [1] SEQUENCE FROM N.A. FT VARIANT 473 474 SEQUENCE 588 AA; 65850 MW; 3D986A7DF5D66B CRC64;

RP MEDLINE-87090408; PubMed=3467201; SEQUENCE FROM N.A. DR
RA Padgett, R.W., St. Johnston, R.D., Gelbart, W.M.; KW
RT "A transcript from a Drosophila pattern gene predicts a protein homologous to the transforming growth factor-beta family."; Nature 325:81-84 (1987).
RN [2] SEQUENCE FROM N.A. DR
RC STRAIN-DP CN BW; KW
RA Richter, B., Long, M., Lewontin, R.C., Nitasaki, E.; RT
RT "Nucleotide variation and conservation at the dpp locus, a gene controlling early development in Drosophila.,"; Genetics 145:311-323 (1997).
RN [3] CHARACTERIZATION, AND SEQUENCE OF 457-476. DR
RA Panambian, G.B.F., Rashka, K.E., Neitzel, M.D., Hoffmann, F.M.; RT
RT "Biochemical characterization of the Drosophila dpp protein, a member of the transforming growth factor beta family of growth factors.,"; Mol. Cell. Biol. 10:2669-2677 (1990).
CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DR
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS TOGETHER WITH SCW. DR
CC SUBUNIT: HETEROODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT. DPP/DPP DR
CC HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN. DR
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES, AND MIDGUT MESENTERM. DR
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. DR
CC -----
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CC -----
CC EMBL; M30116; ARA28482.1; - DR
DR EMBL; U63657; AAC7552.1; - DR
DR PIR; A26158; A26158. DR
DR FlyBase; FBgn000090; dpp. DR
DR HSSP; P12643; 3BMP. DR
DR InterPro; IPR01835; TGFb. DR
DR InterPro; IPR01111; TGFb_N. DR
DR Pfam; PF00019; TGF-beta_1. DR
DR Pfam; PF00688; TGFb_propeptide; 1. DR
DR ProDom; PDD0057; TGFb; 1. DR
DR SMART; SM00204; TGFb; 1. DR
DR SMART; SM00204; TGFb; 1.

RESULT 14 DR
ID DECA_DROPS STANDARD PRT; 621 AA. DR
AC P91650; P91650; DR
DT 15-DEC-1998 (Rel. 37, Created) DR
DT 15-DEC-1998 (Rel. 37, Last sequence update) DR
DE Decapentaplegic protein precursor (DPP-C protein). DR
GN DPP. DR
OS Drosophila pseudoobscura (Fruit fly). DR
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; DR
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; DR
OC Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila. DR
OX NCBI_TaxID=7237; DR
RN [1] SEQUENCE FROM N.A. DR
RX MEDLINE-97225212; PubMed=9071585; DR
RA Newfeld, S.J., Padgett, R.W., Findley, S.D., Richter, B.G., Sanicola, M., DR
RA de Cuevas, M., Gelbart, W.M.; RT
RT "Molecular evolution at the decapentaplegic locus in Drosophila.,"; Genetics 145:297-309 (1997). DR
CC -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DR
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE DR
CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL

QY 4 EDESETWDOATGTRKFLYQDIR --- DEGWETLEV --- SSAVKRWRADSTNNKLEV 55
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
294 KDKSKIDDRPHHRRFLHFDVKSIAPADEKUKAELQTRALSQWVARSANRTRYQV 353
QY 56 T----- VQSHRE----- SCDTLDTSVPRG ----- SKNLFVVFS 85
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
354 LVDITIRVGVRGCREPSYLLDFTKVRNLSDTVSDVQPAVDRWLSPQRNQGLLVEVR 413
QY 86 NDHS----- NTKTRDLIKEMIGHEBTMLVKTAKNAYQAGESOEEBDLGYTAV 138
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
414 TVRSILKPAHHVRLRKSADAEHRMWHQKQLFTTDDGRHK ARSTRDVSQGGGGKG 472
QY 139 GPLLARRRSTGASSH --- CORTSLVNFDIGWOSWITLAPKEYDAYECKGCCFFPLADD 195
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
473 GRNKKRQPRPRTRRKNHDTCRRHSLYVDFSDVGHWDWIVAPLGDAYYCHGKCPFFPLADH 532
QY 196 VTPPKHAWOTVHLLKPTKVGKACCVPTKLSPPSILYKDMGPTLXHYEGMSVAECG 255
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
533 FNSTINHAWVOTLWNMNPFGKVKPACCVPTQLDSVAMLYLNDQSTVVLK-NYQEMTVVCG 591
QY 256 CR 257
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
592 CR 593

Search completed: April 2, 2003, 14:50:07
Job time : 28 secs

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model
Run on: April 2, 2003, 14:47:35 ; Search time 44 Seconds

Title: US-10-002-278-9
Perfect score: 1368

Sequence: 1 DVLEDSETWDQAGTGTKFLV.....GVPTLKYHEGMSVAECGCR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%,
Maximum Match 100%,
Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	808.5	59.1	427	2 A40735	TGF beta homolog d
2	34.5	25.2	408	1 BMHU6	bone morphogenetic
3	34.2	25.0	408	2 S3343	bone morphogenetic
4	34.1	24.9	408	2 S58791	bone morphogenetic
5	33.7.5	24.7	420	2 I40541	bone morphogenetic
6	33.0	24.1	436	2 B54542	cartilage-derived
7	32.7.5	23.9	405	2 I50608	bone morphogenetic
8	32.7.5	23.9	408	2 JH0801	bone morphogenetic
9	326.5	23.9	400	2 A49479	bone morphogenetic
10	32.5	23.8	588	2 A26158	decpentapleic pr
11	31.9	23.3	398	2 JH0688	bone morphogenetic
12	31.8	23.2	398	2 JH0687	bone morphogenetic
13	316.5	23.1	401	2 JH0689	bone morphogenetic
14	314.5	23.0	430	2 J01184	osteogenic protein
15	31.4	23.0	393	2 S37073	bone morphogenetic
16	31.3	22.9	394	2 S45355	bone morphogenetic
17	312.5	22.8	454	1 BMHU5	bone morphogenetic
18	31.2	22.8	125	2 S43295	bone morphogenetic
19	31.1	22.7	396	1 BMHU2	bone morphogenetic
20	310.5	22.7	313	2 I51284	bone morphogenetic
21	310.5	22.7	461	2 S55408	spdynl protein - s
22	308	22.5	501	2 A55452	cartilage-derived
23	307	22.4	353	2 I50607	bone morphogenetic
24	307	22.4	501	2 JC2347	bone morphogenetic
25	305.5	22.3	431	1 BMHU7	growth/differentia
26	305.5	22.3	452	2 I4942	bone morphogenetic
27	305.5	22.3	495	2 S43394	bone morphogenetic
28	301	22.0	402	2 A44056	osteogenic protein
29	301	22.0	510	2 A54798	vg-1-related prote

ALIGNMENTS

RESULT 1

A40735
TGF beta homolog dsl-1 - chicken

C;Species: Gallus gallus (chicken)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

R;Basler, K.; Edlund, T.; Jessell, T.M.; Yamada, T.

Cell 73, 687-702, 1993

A;Title: control of cell pattern in the neural tube: regulation of cell differentiation

A;Reference number: A40735; MUID:93272310; PMID:916556

A;Accession: A40735

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-427 <BAS>

A;Cross-references: GB1L12032; NID:9304379; PIDN:AAA48752.1; PMID:9304380

A;Experimental source: spinal cord

A;Note: sequence extracted from NCBI backbone (NCBIN:132680, NCBIPI:132681)

C;Superfamily: inhibin

Query Match 59.1%; score 808.5; DB 2; Length 427;
Best Local Similarity 61.9%; Pred. No. 4e-62; Mismatches 9; Indels 5; Gaps 5;

Matches 161; Conservative 31; Mismatches 59; Description

Qy 1 DVLEDSETWDQAGTGTKFLV.....GVPTLKYHEGMSVAECGCR 257
Db 174 DLV-DGDRWENKSTSKLIVSISDQGWENFESAVKWWKADKMTKNNKLEWTEK 232

Qy 61 RES--CDTLDISYPGSKNLPFFVVSNDRNGKTREDLKLKEIGHEQETMLVKTAK 117
Db 233 DLSDFPGCGKLDTWTHDKNLLTIVFNSDNGKETKVE-LKEMIVHEQSSVLNGK 291

Qy 118 NAYGAGESQEEGLDGTVAVGPLATRKRTGASSHCKTSLSRVNFEDIGWMSWIIAPK 177
Db 292 NDSSEEEQFREKAI--ARPPQHSSRSKRSIGA-NHCRRTSLAVNREIGWMSWITAPK 347

Qy 178 FYDAVECKGGCFPLADDVTPKHAUTVOTLHKKPFKVKACCVPTKSPISLYKUDM 237

Qy 348 DYAEFECKGGCFPLIDNTVTPKHAUTVOTLHQLQPKKACCVPTKIDAIILYKDA 407

Qy 238 GVPTLKYHEGMSVAECGCR 257
Db 408 GVPTLKYHEGMSVAECGCR 427

bone morphogenetic
bone morphogenetic
bone morphogenetic
Vg1 embryonic - Ca
gene nodal protein
vgr protein - rat
TGF-beta-related p
bone morphogenetic
growth/differentia
bone morphogenetic
bone morphogenetic
transforming growt
bone morphogenetic
GDF-1 embryonic gr
activin betta-A cha

R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsick, L.M.; Whitters, M.J.; Krieg, R.W.;

Search completed: April 2, 2003, 14:52:31
Job time : 45 secs

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GenCore version 5.1.4-p5-4578

Om protein - protein search, using sw model

Run on: April 2, 2003, 14:51:46 ; Search time 36 Seconds

436.443 Million cell updates/sec

Title: US-10-002-278-9

Perfect score: 1368

Sequence: 1 DVLEDSETWDQATGKTFLV.....GVPTIYHYEGMSVAECGCR 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

Published Applications AA: *

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1: /cgn2_6/ptodata/2/pubpaas/us08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaas/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaas/us06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaas/us07_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaas/us07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaas/us07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaas/PCTVS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaas/us08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaas/us09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaas/us10_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaas/us10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaas/us10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaas/us60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaas/us60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	1368	100.0	257	12 US-10-002-278-9
2	808.5	59.1	427	12 US-10-002-278-2
3	516.5	37.8	425	9 US-09-813-398-32
4	361	26.4	419	10 US-09-813-398-32
5	354	25.9	437	10 US-09-784-911-4
6	350	25.6	427	10 US-09-784-911-6
7	349.5	25.5	321	9 US-09-945-822-26
8	345	25.2	408	9 US-09-804-625-6
9	345	25.2	408	10 US-09-749-728B-69
10	345	25.2	409	9 US-09-813-398-27
11	337.5	24.7	263	9 US-09-945-822-32
12	334.5	24.5	411	9 US-09-945-822-28
13	330	24.1	435	10 US-09-730-772-14
14	330	24.1	436	10 US-09-735-849-14
15	322	23.5	451	10 US-09-784-911-10
16	320	23.4	433	10 US-09-784-911-8
17	313	22.9	433	12 US-09-784-911-12
18	312.5	22.8	455	9 US-09-813-398-28
19	312	22.8	435	10 US-09-784-911-14

RESULT 1

US-10-002-278-9

; Sequence 9, Application us/10002278

; Patent No. US200201323341

; GENERAL INFORMATION:

; APPLICANT: Jessell, Thomas M.

; APPLICANT: Basler, Konrad

; APPLICANT: Yamada, Toshiya

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1

; FILE REFERENCE: 05754314-A

; CURRENT APPLICATION NUMBER: US/10/002,278

; CURRENT FILING DATE: 2001-11-02

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 9

; LENGTH: 257

; TYPE: PRT

; ORGANISM: Mouse

US-10-002-278-9

Query Match Best Local Similarity

100.0%; score 1368; DB 12; Length 257;

Matches 257; Conservative 0; Mismatches 0; Pred. No. 2.e-128; Indels 0; Gaps 0;

QY 1 DVLEDSETWDQATGKTFLVSDIDRGWWEILVSSAVKWRADSTWNKLEVYQSH 60

QY 1 DVLEDSETWDQATGKTFLVSDIDRGWWEILVSSAVKWRADSTWNKLEVYQSH 60

QY 61 RESCDTLDSPVPSKSNLPPFVFSNDRSNSNGKTRFLDILKEMIGHEQETMVKTAQWY 120

QY 61 RESCDTLDSPVPSKSNLPPFVFSNDRSNSNGKTRFLDILKEMIGHEQETMVKTAQWY 120

Db 61 RESCDTLDSPVPSKSNLPPFVFSNDRSNSNGKTRFLDILKEMIGHEQETMVKTAQWY 120

Db 61 RESCDTLDSPVPSKSNLPPFVFSNDRSNSNGKTRFLDILKEMIGHEQETMVKTAQWY 120

QY 121 OGAGSQQEERGLDGTYAVGLPLAARRKRGASHCOKTSRVNFEDIGMSWATPKED 180

QY 121 OGAGSQQEERGLDGTYAVGLPLAARRKRGASHCOKTSRVNFEDIGMSWATPKED 180

QY 241 TLYVYEGMSVAECGCR 257

Db 241 TLKYHYEGMSVAEGCCR 257

RESULT 2

US-10-002-278-2

Sequence 2, Application US/10002278

Patent No. US2002013234A1

GENERAL INFORMATION:

APPLICANT: Jessell, Thomas M.

APPLICANT: Basler, Konrad

APPLICANT: Yamada, Toshiya

TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1

FILE REFERENCE: 05754034-A

CURRENT APPLICATION NUMBER: US/10/002,278

CURRENT FILING DATE: 2001-11-02

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 427

TYPE: PRT

ORGANISM: Chick

US-10-002-278-2

Query Match Similarity 59.1%; Score 508.5; DB 12; Length 427;

Best Local Similarity 61.9%; Pred. No. 2.4e-72; Matches 161; Conservative 31; Mismatches 59; Indels 9; Gaps 5;

Oy 1 DVLESESETMQATEKTEIWSQD--RDEGWTLEVSANVKRWRADSTNNKLEVTVQ 58

Db 170 EVLE-SKGDNEGERNMLVLSVYGTGNTSEWTFDVTARWQSGST--HOLEVHIE 226

Oy 59 S-HRESCDT--LDISVPPGSKNLPFFVWSNDRNGTKTRDLIKEMIGHQETMLV 113

Db 227 SKHDAEDSGRABIDSAQHNHPLWVSDQG--SDKERKELNEMTSHQPLP 283

Oy 114 KTAKNAYQGAGESQEEGLGYAVGP---LLARRK-----RSTGASSHCQTS 159

Db 284 -----DNLGUDSFSS-GPGEAELQMSNNTIDSTARIRRANKGKQCRP 328

Oy 160 LRVNFEDIGDWSITAPKEYDAVECKGCGCFPLADDVPTKHAIVOTLVHLKFPVKGKA 219

Db 329 LYDKEIGNDWSITAPKEYDAVECKGCGCFPLADDVPTKHAIVOTLVHLKFPVKGKA 388

Oy 220 CCVPKRLSPISLTKDDMVGPTKHYEGMSVAEGCCR 257

Db 389 CCVPKRLSPISLTKDDMVGPTKHYEGMSVAEGCCR 425

RESULT 3

US-09-813-398-32

Sequence 32, Application US/09813398

Patent No. US2002016929A1

GENERAL INFORMATION:

APPLICANT: Harrison, Leonard C.

APPLICANT: Jiang, Fang-Xu

APPLICANT: Stanley, Edouard Guy

APPLICANT: Gonez, Leonel Jorgé

TITLE OF INVENTION: Pancreatic islet cell growth factors

FILE REFERENCE: Davies, Collison Cave

CURRENT APPLICATION NUMBER: US/097784,911

CURRENT FILING DATE: 2001-09-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 2.1

SEQ ID NO 2

LENGTH: 419

TYPE: PRT

ORGANISM: mouse

FEATURE:

NAME/KEY: UNSURE

LOCATION: (186)

OTHER INFORMATION: Xaa at position 186 is Tyr or His

US-09-784-911-2

Query Match Similarity 26.4%; Score 361; DB 10; Length 419;

Best Local Similarity 37.1%; Pred. No. 8.6e-28; Matches 88; Conservative 32; Mismatches 75; Indels 42; Gaps 8;

Oy 29 WETLVESSAKRWRADSTNNKLEV---VOSIRESCDTLDSVPPCSK---LRF 80

Db 217 WETEVSPAVLWTRKPKPNYGAIEVTHLHOTRTHQGQVTRSPSPPGSDMAOLPL 276

Oy 81 FVVFSDNDRNGTKTRDLIKEMIGHQETMLVTKANAVOGAGESQEEGLGYTAVGP 140

Db 277 LYTCRHDGR-----GH-----TTRRRAKRSRKPRQREBEM-----P 308

PRIOR APPLICATION NUMBER: PCT/US99/05908

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: PCT/US98/19772

FILING DATE: 1998-09-22

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSeq for Windows version 4.0

SEQ ID NO 32

LENGTH: 425

TYPE: PRT

ORGANISM: HOMO SAPIEN

US-09-813-398-32

RESULT 5

US-09-784-911-4

Sequence 4, Application US/09784911

Query Match

37.8%; Score 516.5; DB 9; Length 425;

Patent No. US20020072115A1
 GENERAL INFORMATION:
 APPLICANT: Harrison, Leonard C.
 APPLICANT: Jjiang, Fang Xu
 APPLICANT: Stanley, Edouard Guy
 TITLE OF INVENTION: Pancreatic islet cell growth factors
 FILE REFERENCE: Davies Collision Cave
 CURRENT APPLICATION NUMBER: US/09/784,911
 CURRENT FILING DATE: 2001-09-17
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: Patentin version 2.1
 SEQ ID NO 4
 LENGTH: 437
 TYPE: PRT
 ORGANISM: mouse
 FEATURE:
 LOCATION: (186)
 OTHER INFORMATION: Xaa at position 186 is Tyr or His

US-09-784-911-4
 Query Match 25.9%; Score 354; DB 10; Length 437;
 Best Local Similarity 37.7%; Pred. No. 4.6e-26; Mismatches 93; Indels 30; Gaps 6;
 Matches 90; Conservative 26; Mismatches 93; Indels 30; Gaps 6;
 QY 29 WETLVEVSSAVKRVRAUDSTTKNKLVEV---VWSHRESCDTLISVPGPSK---LPP 80
 DB 217 WETFDVSVAVLRLTREKOPNGLALVTHHQTRTHOGHVRISRLSPGSGWQLRPL 276
 QY 81 FVFSNSDNGKETRDLKEMIGHEQETMLVKI---AKNAVQAGSESQEERGLDQTA 137
 DB 277 LVFGHD-GRGHILTRRRAKSSPKHHPORSTRQEOKL-----SEED----- 317
 QY 136 TAVGPLLARRKRGSTGASSHCKTSLVNFEDIGMSWILAPKEVDAYBCKGCFPLADD 195
 DB 318 -----LTKK---NNCRKHSLSVDFSDGWNDWIVAPPQIQAFTCHGDCPPFLADH 367
 QY 196 VTPTKHAWOTVHLKPTKVKGKACVPTKLSPIVLYKDDMCPYTLVYHBCMSVAECG 255
 DB 368 INSTNHALVOTLVN-SVNSSIPKACVPTLELSAISMLYLDYDVKVL-NYQDVKVPGCG 425
 QY 256 CR 257
 DB 426 CR 427

RESULT 6 US-09-784-911-6
 Sequence 6, Application US/09784911
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Leonard C.
 ; APPLICANT: Jiang, Fang Xu
 ; APPLICANT: Stanley, Edouard Guy
 ; APPLICANT: Gomez, Leonel Jorge
 ; TITLE OF INVENTION: Pancreatic islet cell growth factors
 ; FILE REFERENCE: Davies Collision Cave
 ; CURRENT APPLICATION NUMBER: US/09/784,911
 ; CURRENT FILING DATE: 2001-09-17
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patentin version 2.1
 ; SEQ ID NO 6
 ; LENGTH: 427
 ; TYPE: PRT
 ; ORGANISM: mouse
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (186)
 ; OTHER INFORMATION: Xaa at position 186 is Tyr or His

RESULT 7 US-09-945-182-26
 Sequence 26, Application US/09945182
 Patent No. US2002160494A1
 GENERAL INFORMATION:
 APPLICANT: Celeste, Anthony J.
 Wozney, John
 Rosen, Vicki A.
 Wolman, Neil
 Tomson, Gerald H.
 Melton, Douglas A.
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 Cambridge Park Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/945,182
 FILING DATE: 31-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/808,324
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-945-182-26

Query Match 25.6%; Score 350; DB 10; Length 427;
 Best Local Similarity 36.8%; Pred. No. 1.1e-26; Mismatches 77; Indels 44; Gaps 9;
 Matches 89; Conservative 32; Mismatches 34; Indels 94; Gaps 12;
 QY 29 WLEDSETWD---QATGTTKTFVSVDIRDEGWE-TLEVSSAVKRVRADSTINKLEV 55

QY 2 2 WLEDSETWD---QATGTTKTFVSVDIRDEGWE-TLEVSSAVKRVRADSTINKLEV 55

RESULT 8
US-09-804-625-6
; Sequence 6, Application US/09804625
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; Wozney, John M
; TITLE OF INVENTION: NO. US20030049826A1
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/804,625
; FILING DATE: 09-Mar-2001
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/925,779
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaptos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCED DOCKET NUMBER: 51160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-09-804-625-6

Query Match 25.2%; Score 345; DB 9; Length 408;
Best Local Similarity 35.9%; Pred. No. 3; 3e-26; Gaps 7;
Matches 85; Conservative 28; Mismatches 76; Indels 48;

RESULT 9
US-09-749-728B-69
; Sequence 69, Application US/09749728B
; GENERAL INFORMATION:
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIAC MUSCLE CELLS
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION NUMBER: US/09/749,728B
; CURRENT FILING DATE: 2001-09-17
; PRIORITY APPLICATION NUMBER: H11-372826
; FILE REFERENCE: 00766.00043
; PRIORITY APPLICATION NUMBER: PCT-JP00-01148
; PRIORITY FILING DATE: 2000-02-28
; PRIORITY APPLICATION NUMBER: PCT-JP00-07741
; PRIORITY FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin Ver.2.0
; LENGTH: 408
; SEQ ID NO: 69
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-749-728B-69

Query Match 25.2%; Score 345; DB 10; Length 408;
Best Local Similarity 35.9%; Pred. No. 3; 3e-26; Gaps 7;
Matches 85; Conservative 28; Mismatches 76; Indels 48;

RESULT 10
US-09-813-398-27
; Sequence 27, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szekulinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS

QY 81 FVFSNDRSNGTKTRDOLIKEMTGHEOTMLVKTAKNAYOGAGESQEERGLDQYTAVGP 140
Db 272 LVTFGHD-GHGHALTRRRRAKRSRPHHSQR----- 300
QY 141 LLLRKRSRGASHCQKTSLSLRVNPEDIGDWSNITAPKEYDAYECKGGCFPLADDVTPK 200
Db 301 .-ARKK---NNKRRRHSLSVPSDVGNDWIVAPPGYQAFYCHGDCPPLADHLNST 353
QY 201 HAIVOTLVLKPKVKGACCVTKLSPSILYKDDMGVPLKLYVYEGMSVAEGCR 257
Db 354 HAIVOTLVLN-SVNSSIKACCVIELSALISMILDEDKVVLK-NIÖEMVVEGGCR 408

QY 56 TVOSRRECDTLDISVPGSKN-----FVFSNDRSNGTKTRDOLIKEMTGHEOTMLVKTAKNAYOGAGESQEERGLDQYTAVGP 113
Db 114 RARGPOQ-----PPPDRLSLGFGGRVRVRPQERALLVVE-----TRSQRNLFAEM 159
QY 104 IGHEOTMLVKTAKNAYOGAGESQEERGLDQYTAVGP-----ARRKSTGASSH----- 154
Db 160 --REQ---LGSAAAGGAGAAGSWSWPPSPGARPLWSPGRARRTAFAFLASHLEPTNHAIQTL 213
QY 155 ---COKTSLRNFDIGDWSNITAPKEYDAYECKGGCFPLADDVTPKHAIVQTVL 208
Db 214 KKSRLRCSKRPLAHNKEGLWDWMTAPLEYAVHCGVCDPFLASHLEPTNHAIQTL 273
QY 209 HLLKEPTKVKRACKCVPTKLSPLSITLYKDDMGVPLKLYVYEGMSVAEGCR 257
Db 274 NSMDRGSSTPPSCCVPTKLTPIISLY-1DAGNNWVQYEDMVAEVSCGCR 321

FILE REFERENCE: UOFMD-003C1
 CURRENT APPLICATION NUMBER: US/09/813,398
 CURRENT FILING DATE: 2001-03-20
 PRIORITY NUMBER: PCT/US99/05908
 PRIORITY FILING DATE: 1999-03-19
 PRIORITY APPLICATION NUMBER: PCT/US98/19772
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FASTSEQ for Windows version 4.0
 SEQ ID NO: 27
 LENGTH: 409
 TYPE: PRM
 ORGANISM: HOMO SAPIEN
 US/09-813-398-27

Query Match 25-28: Score 345; DB 9; Length 409;
 Best Local Similarity 35.9%; Pred. No. 3.3e-26; Indels 48; Gaps 7;
 Matches 85; Conservative 28; Mismatches 76;

Query Match 29 WETLENSAVVWRADSTNKLNKLEUT---VYSHRSRCDTIDISVPPGSN---LPF 80
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 16 KTRIVSDIDRQKWE--TLEVSAYKRMVRADSTNKLNKLEUTVYSHRSRCDTIDISV-- 71
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 25 KSFDFWQGLRPWPWKQCLCLERAA--WGELXGDTGARARGQQP---PPFLDLRSIG 76
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 277 FGRRVRVPRQERAI-LVVF-----TRQSRKIFTEM-HEC-----LGSAE 113
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 126 SQEEGL---DGTYAVGPILL---ARRKRSTGASSH-----CQRTSLRVNFED 166
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 114 AGAGAEGSCPAPSGSPGSPGWSLSPGRRRRTAFASRHKGRHKRSRLRCSPKLPVNFKE 173
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 167 IGDMSWIIKPQKDYAFCKGGCCFLADDVTPKTHAIQVOTLWILKFPITKVGKACCPYKL 226
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 174 IGDWDWIIAPLIEVYHCEGVCDFPLRSIHLPEPTNHAIOTLWMSMDPGSTPPSCCVPTKL 233
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 227 SPISILYKDDMKSCPYTKIHYFGMSVACGCR 257
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 234 TPISILY-IDAGNNKXYYKQYEDMVWESCGR 263
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

RESULT 11
 US/09-945-182-32
 Sequence 32, Application US/09945182
 Patent No. US20020160494A1
 GENERAL INFORMATION:
 APPLICANT: celeste, Anthony J.
 Wozney, John
 Rosen, Vicki A.
 Wolfman, Neil
 Thomson, Gerald H.
 Melton, Douglas A.
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/945,182
 FILING DATE: 31-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/808,324
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Laza, Steven R.
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-D
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 263 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US/09-945-182-32

Query Match 24-78: Score 337.5; DB 9; Length 263;
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 16 KTRIVSDIDRQKWE--TLEVSAYKRMVRADSTNKLNKLEUTVYSHRSRCDTIDISV-- 71
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 25 KSFDFWQGLRPWPWKQCLCLERAA--WGELXGDTGARARGQQP---PPFLDLRSIG 76
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 114 AGAGAEGSCPAPSGSPGSPGWSLSPGRRRRTAFASRHKGRHKRSRLRCSPKLPVNFKE 173
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 167 IGDMSWIIKPQKDYAFCKGGCCFLADDVTPKTHAIQVOTLWILKFPITKVGKACCPYKL 226
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 174 IGDWDWIIAPLIEVYHCEGVCDFPLRSIHLPEPTNHAIOTLWMSMDPGSTPPSCCVPTKL 233
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 227 SPISILYKDDMKSCPYTKIHYFGMSVACGCR 257
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

Query Match 234 TPISILY-IDAGNNKXYYKQYEDMVWESCGR 263
 Best Local Similarity 35.4%; Pred. No. 9.8e-26; Indels 61; Gaps 12;
 Matches 96; Conservative 28; Mismatches 86;

TELEPHONE: 617 438-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 411 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 US-09-945-182-28

Query Match 24.5%; Score 334.5; DB 9; Length 411;
 Best Local Similarity 32.0%; Pred. No. 3.7e-25;
 Matches 83; Conservative 32; Mismatches 85; Indels 59; Gaps 8;

Qy 17 TFLVNSQDTIRDEGMEVTELVSSAVKRWYRADSTTNKLNKLETVQSHRESCOTLDISVPPGSK 76
 Db 194 TRLYNQNA--SRRESFVTPAVMRWTAQGHANHGTVWYAHLEEKQGSKRHRI--SR 248
 Qy 77 NL--PFPVVFSSDRNGTKETRFLDLKEMIGH---EDBTML--VKTAKN 118
 Db 249 SLDQDEHWSQSRPPLVTFGDK-----GHPLHKRERKRTALAGRTPAQ 293
 Qy 119 AYOGAGESOEEERGLGDYTAVGPLLARRKRSINGASSHCKTSRLRVNFEDIGWDSWIAKPE 178
 Db 294 SGGGAGGRGHRGRC-----RSRCSRKRPLHVDFKELGWDWIAPLD 333
 Qy 179 YDAECKGGCFPLADDVTPKTHATVOTLWHLKFPTKVSKACCPVPTKUSPISIPLYKDMG 238
 Db 334 YEAHCEGICDPLRSLEPTNHAIQTQLNNSMAPDAAPSCCVPARLSPISIPLYIDAAN 393
 Qy 239 VPTLKYHVEGMSVAECCR 257
 Db 394 NVVYK-QYEDMVVEACCCR 411

RESULT 13
 US-09-730-772-14

Sequence 14 Application US/09730772
 Patent No. US201001131A1

GENERAL INFORMATION:
 APPLICANT: Luyten, Frank P.
 APPLICANT: Moos, Jr., Malcolm
 APPLICANT: Chang, Steven Chao-Huan
 TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
 NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, 16th Floor
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92660

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/730,772
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Barfield, Neil S
 REGISTRATION NUMBER: 39,901
 REFERENCE/DOCKET NUMBER: NTH099.001APC
 APPLICATION NUMBER: 08/836,081
 FILING DATE:

PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Barfield, Neil S
 REGISTRATION NUMBER: 39,901
 REFERENCE/DOCKET NUMBER: NTH099.001APC

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-235-8550
 TELEFAX: 619-235-0176

SEQUENCES CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid

RESULT 14
 US-09-735-849-14

Sequence 14 Application US/09735849
 Patent No. US201001701A1

GENERAL INFORMATION:
 APPLICANT: Luyten, Frank P.
 APPLICANT: Moos, Jr., Malcolm
 APPLICANT: Chang, Steven Chao-Huan
 TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
 NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92660

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows

SOFTWARE: FASSEQ FOR Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/735,849
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/836,081
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Barfield, Neil S
 REGISTRATION NUMBER: 39,901
 REFERENCE/DOCKET NUMBER: NTH099.001APC

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-235-8550
 TELEFAX: 619-235-0176

SEQUENCES CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-09-730-772-14

Query Match 24.1%; Score 330; DB 10; Length 436;
 Best Local Similarity 36.7%; Pred. No. 1.1e-24;
 Matches 81; Conservative 23; Mismatches 67; Indels 50; Gaps 7;

Qy 72 PPGSKNLPF-----FVVFNSDRNGTKETRFLDLKEMIGH---EDBTML--VKTAKN 119
 Db 231 PPDLSLGRGRVTPQERALIVWERSQ-----RKTFLAFMREGQSATEVV----- 278
 Qy 120 YQGAGESOEEG-----LDGYAVG--PLIARRKRSTGASSH-----CQ 156
 Db 279 --GGGGAGGSGCPRPPPPPPPPGSGTDAQWMSPPSGRRTAFAFSRHKRGKKSRLCS 336
 Qy 157 KTSLRVNEBDIGNSWIAKPEYDATECKGGCFPLADDVTPKTHATVOTLWHLKFPTKVSKACCPVPTKUSPISIPLYKDMG 216
 Db 337 KKLPHVNHKEGLWDWIAPLEYEAHCEGICDPLRSLEPTNHAIQTQLNNSMDPST 396
 Qy 217 GKA CCPVPRKLSPIPSLKKDDMKGVPTKHYEGMSVAECCR 257
 Db 397 PPSCCVPKRPTPSILY-IDQGNVNVINE1BEMWVESCGR 436

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GenCore version 5.1.4-p5-4578

Om protein - protein search, using sw model

Run on: April 2, 2003, 14:40:05 ; Search time 75 seconds (without alignments)

456,605 Million Cell updates/sec

Title: US-10-002-278-9

Perfect score: 1368

Sequence: DVLEDSETWDQATGKTFPLV.....CVPTILKYHFGMSVAECGCR 257

Scoring table: BLOSUM62

gapop 10.0 , gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_101002:*

1: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS2/gcdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS2/gcdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcdata/geneseq/geneseq-emb1/AA2002.DAT:*

RESULT 1

1: AAR31372

ID AAR31372 standard; Protein; 428 AA.

XX

AC AAR31372;

XX

DT 24-JUN-1993 (first entry)

XX

DE Murine bone morphogenic protein-9 (BMP-9).

XX

KW bone formation; cartilage formation; wound healing; tissue repair; surgery; fracture treatment; periodontal disease; osteoporosis; increase neuronal survival; transplantation; nerves; nervous system.

XX

COS MUS musculus.

XX

FEW

FT Key location/Qualifiers

FT Protein 319..427

FT Label= mature peptide

XX

W09300432-A.

XX

FD 07-JAN-1993.

XX

PF 25-TUN-1992; 922W0-US05374.

XX

PR 25-JUN-1991; 911US-0720590.

XX

(GENY) GENETICS INST INC.

XX

PI Celeste AJ, Wozney JM;

XX

DR WPI: 1993-036379/04.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1336.5	97.7	428	14 AAR31372	Marine bone morpho
2	1336.5	97.7	428	17 AAR86505	Marine bone morpho
3	1336.5	97.7	428	21 AAY82271	Marine bone morpho
4	1146.5	83.8	429	22 AAE1210	Albumin fusion pro
5	1146.5	83.8	429	22 AAU14195	Human novel protei
6	1146.5	83.8	429	22 AAU1431	Human novel protei
7	808.5	59.1	427	16 AAR8607	Dorsalin I. Gallu
8	634	46.3	150	17 AAR86503	Human BMP-9 polyope
9	619	45.2	150	21 AAY82272	Human bone morpho
10	619	45.2	150	14 AAR31374	Human bone morpho

FT /label= Signal
 FT 319..428
 FT /label= Bone_morphogenetic_protein-9
 XX
 PN US6034062-A.
 PR ID AAE12410
 XX ID AAE12410 standard; Protein; 429 AA.
 PD AC
 XX AC
 PR XX
 XX 13-MAR-1997; 97US-0815652.
 XX
 PR 13-MAR-1997; 97US-0815652.
 XX
 PA (GENE) GENETICS INST INC.
 XX
 PI Thies RS, Song JJ;
 XX
 DR WPI; 2000-255707/22.
 DR N-PSDB; AAZ95746.
 XX
 PT Novel bone-morphogenetic protein (BMP)-9 polypeptides, useful in the treatment of bone and cartilage defects and in wound healing and tissue repair, as well as hepatic growth and function -
 XX
 PS Claim 1; column 33-36: 36pp; English.
 XX
 CC A method has been developed for decreasing proliferation of kidney or lung epithelial cells, or for inhibiting kidney tubule formation, in a patient. The method comprises administering an amount of a bone morphogenetic protein 9 (BMP-9) protein. BMP-9 polypeptides from the invention may be used to induce bone and cartilage formation or other connective tissue formation, in periodontal disease, in wound healing and tissue repair, hepatic growth and function, and in regulating lung and kidney cell function. The polypeptides can be used for healing of bone fractures, open fracture reduction, improved fixation of artificial joints, tooth repair processes, treatment of osteoporosis and osteoarthritis, and as a dietary supplement or as a component of cell culture media. BMP-9 may also be used for repair and regenerating of liver cells. The BMP-9 polypeptides may also have angiogenic, chemotactic and/or chemoattractant properties, and may induce collagen synthesis, fibrosis, differentiation processes, cell proliferative responses, cell adhesion responses, and migration. When dimerized, the BMP-9 polypeptide is expected to demonstrate effects on the production of follicle stimulating hormone (FSH), and so may be used as a contraceptive, as a fertility inducing therapeutic, and for advancing the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals. The present sequence represents murine BMP-9.
 XX
 Sequence 428 AA:
 XX
 Query Match 97.7%; Score 1336.5; DB 21; length 428;
 CC Best Local Similarity 98.4%; Pred. No. 9.9e-129;
 CC Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 CC
 OY 1 DVLDEDSETWDQATGKTPFLVSODIRDEGWTLEYSSAVKRWRADSTTKNKLFVWOSH 60
 DB 173 DVLEDSETWDQATGKTPFLVSODIRDEGWTLEYSSAVKRWRADSTTKNKLFVWOSH 232
 OY 61 RESDTDISVPGSKNLUPEFVVFNSDRNSNCTKTRDLDLKEIMGHEQTMVWTKAY 120
 DB 233 RESCDTDISVPGSKNLUPEFVVFNSDRNSNCTKTRDLDLKEIMGHEQTMVWTKAY 291
 OY 121 QGAGESQEEGLGYTAVGPLARRRSTGASSCQTSURVNEPDIGDSWIAPEKD 180
 DB 292 QVAGESQEEGLGYTAVGPLARRRSTGASSCQTSURVNEPDIGDSWIAPEKD 351
 OY 181 AYECKGCFPLADDVPTKHAIVQTLVHLKFPTRKVGACCVPKLSPISILYKDDMGVP 240
 DB 352 AYECKGCFPLADDVPTKHAIVQTLVHLKFPTRKVGACCVPKLSPISILYKDDMGVP 411
 OY 241 TLKIHEGMSVABGCR 257
 DB 412 TLKIHEGMSVABGCR 428

Query Match 83.8%; Score 1146.5; DB 22; length 429;
 CC Best Local Similarity 82.9%; Pred. No. 3.6e-109;
 CC Matches 213; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.

XX
SQ Sequence 429 AA;
Query Match 83.8%; Score 1146.5; DB 22; Length 429;

QY	1	DYLEDSEWWQDQATCTKTYLVSQDIDREGWETLEVSSAVKRWRASTDNTNNKLNKLEVYQSH
Db	174	DYLDCTDANDSATETKTYLVSQDIDQBGWETLEVSSAVKRWRASTDNTNNKLNKLEVYQSH
QY	61	RESQDLDISVPPGSKNLPFVVFSNDRNSNGKTREDLKLMEIGHEQETMLVTKTAKAY
Db	234	RKGCDTLDISVPPGSRNLPFVVFSNDRNSNGKTREDLKLMEIGHEQETMLVTKTAKAY
QY	121	QGAGESQEEBGLDGTYAVGPLLARKRKGSTGASSHCQKTSLSRNFEDIGWDSWILAPKED
Db	293	TEAGSSHSHEDTQHVAAGSTLBRKRSAGAGSHCQXTSLRVNFEDIGWDSWILAPKEVE
QY	181	AYECKGCGTFLADDVTPKTHATVOTLVHLKPTKVKGACCOVPTKLSPLSILYKDMGV
Db	353	AYECKGCGTFLADDVTPKTHATVOTLVHLKPTKVKGACCOVPTKLSPLSILYKDMGV
QY	241	TLKYHEGMSVAECGCR
Db	413	TLKYHEGMSVAECGCR
	429	

RESULT 5
AAU14195
ID AAU14195 standard: protein: 429 AA

XX
AC
XX
AAU14195;

BT 24-OCT-2001 (first entry)
XX
DE Human novel protein #66.
XX

KW Human; novel protein; **Anti**anaemic; osteopathic; antiinflammatory; immunomodulatory; cytotoxic; neuroprotective; **vulnerary**; nootropic; anticonvulsant; antiarrhythmic; cereoprotective; antifungal; antiviral

KW antibiotherapy; antiallergic; dermatological; haemostatic; antiinflammatory;
thrombolytic; immunological; antibody; gene therapy; neurotoxicological; antiinfective;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder

PN WO200155437-A2.
XX
PDD
XX
XX
02-AUG-2001.

PP 25-JAN-2001; 2001W0-US02623.
XX PR 25-JAN-2000; 2000US-0491404.

XX
PA
XX
PT
Tara
VTR.
1411 C
Drmnanc
RN.

XX 2001-451939/48.
DR N-PSBB; RAS2200.

XX PT Isolated polypeptides useful for treating anti-inflammatory diseases, PT nervous system disorders, and for regenerating bone and cartilage - XX

PS Example 4; Page 561-562; 894pp; English.
XX
CC The invention relates to polynucleoildes encoding novel human

CC proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant processes of a mammal under the direction of unctors or by the administration of antibodies.

proteins, expression of activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the CC polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to

XX WPI; 2001-451939/48.
DR N-FSDB; AAS22736.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,

PT nervous system disorders, and for regenerating bone and cartilage -

XX Example 4; Page 812-813; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production.

The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies, elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands.

Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, and anti-inflammatory diseases, nervous system disorders, and infection.

The present sequence represents a protein of the invention.

CC Sequence 429 AA;

CC Query-Match 83.8%; Score 1146.5; DB 22; Length 429;

CC Best Local Similarity 82.9%; Pred. No. 3.6e-109; Matches 213; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

CC Qy 1 DVEDESDWQDGATGKFLPSQDIREGATLLESSAVKRVWRADSTNKNLKLEVTVQSH 60

Db 174 DVLGDGTQDWSATETKFLVQSDIDQEGWMEPEVSAKRVWRADSTSKNLKLEVTVESK 233

CC Qy 61 RESCDTLDISVPGSKNLPLFVVFNSDRNSGKTTRDILIKEIGHEETMLVKTAKAY 120

Db 234 RKGCDTLDISVPGSKNLPLFVVFNSDRNSGKTTRDILIKEIGHEETMLVKTAKAY 120

CC Qy 121 QGAGESQEEGGLGYAVGPILLRKSTGASSHQCKTSILRVNFEDIGMSWIAPEYD 180

Db 293 TEAGGESSHEEDTGHVAGSTLARRKSAGSHGSKTSLRVNFEDIGMSWIAPEYE 352

CC Qy 181 AYCKGGGFFPLADDVPTKHAIVOTLVHKKPTKVKGACCVPTKLSPLSILKDDMGP 240

Db 353 AYBCKGGCFFPLADDVPTKHAIVOTLVHKKPTKVKGACCVPTKLSPLSILKDDMGP 412

CC Qy 241 TLYHYEGMSVACGCCR 257

Db 413 TLYHYEGMSVACGCCR 429

CC Sequence 429 AA;

CC Query-Match 83.8%; Score 1146.5; DB 22; Length 429;

CC Best Local Similarity 82.9%; Pred. No. 3.6e-109; Matches 213; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

CC Qy 1 DVEDESDWQDGATGKFLPSQDIREGATLLESSAVKRVWRADSTNKNLKLEVTVQSH 60

Db 174 DVLGDGTQDWSATETKFLVQSDIDQEGWMEPEVSAKRVWRADSTSKNLKLEVTVESK 233

CC Qy 61 RESCDTLDISVPGSKNLPLFVVFNSDRNSGKTTRDILIKEIGHEETMLVKTAKAY 120

Db 234 RKGCDTLDISVPGSKNLPLFVVFNSDRNSGKTTRDILIKEIGHEETMLVKTAKAY 120

CC Qy 121 QGAGESQEEGGLGYAVGPILLRKSTGASSHQCKTSILRVNFEDIGMSWIAPEYD 180

Db 293 TEAGGESSHEEDTGHVAGSTLARRKSAGSHGSKTSLRVNFEDIGMSWIAPEYE 352

CC Qy 181 AYCKGGGFFPLADDVPTKHAIVOTLVHKKPTKVKGACCVPTKLSPLSILKDDMGP 240

Db 353 AYBCKGGCFFPLADDVPTKHAIVOTLVHKKPTKVKGACCVPTKLSPLSILKDDMGP 412

CC Qy 241 TLYHYEGMSVACGCCR 257

Db 408 GVPTLKIVYEGMSVACGCCR 427

CC Sequence 429 AA;

CC Query Match 59.1%; Score 808.5; DB 16; Length 427;

CC Best Local Similarity 61.9%; Pred. No. 2.2e-74; Matches 161; Conservative 31; Mismatches 59; Indels 9; Gaps 5;

CC Qy 1 DVEDESDWQDGATGKFLPSQDIREGATLLESSAVKRVWRADSTNKNLKLEVTVQSH 60

Db 174 DVLGDGTQDWSATETKFLVQSDIDQEGWMEPEVSAKRVWRADSTSKNLKLEVTVESK 233

CC Qy 61 RESCDTLDISVPGSKNLPLFVVFNSDRNSGKTTRDILIKEIGHEETMLVKTAKAY 120

Db 233 DLSPFPCGKLTDTVTHDKNPLTLLVPLTNSDRNSGKTTRDILIKEIGHEETMLVKTAKAY 291

CC Qy 118 NAYGAGESQEEGGLGYAVGPILLRKSTGASSHQCKTSILRVNFEDIGMSWIAPEYD 177

Db 292 NDSSSEEEOREKAI--ARRQHSSRSKRSIGA-NHCRRTSLHNFKEIGMSWIAPEYD 347

CC Qy 178 EYDAVECKGGCFFPLADDVPTKHAIVOTLVHKKPTKVKGACCVPTKLSPLSILKDDMGP 237

Db 348 :D:YAEFECKGGCFFPLADDVPTKHAIVOTLVHKKPTKVKGACCVPTKLSPLSILKDDMGP 407

CC Qy 238 GVPTLKIVYEGMSVACGCCR 257

Db 408 GVPTLKIVYEGMSVACGCCR 427

XX RESULT 7
XX AAR8607
ID AAR8607 standard; Protein: 427 AA.
XX
XX AC AAR8607;
XX DT 02-AUG-1995 (first entry)
XX DE Dorsalin I.
XX KW Dorsalin; neural crest cell differentiation; nerve cells; neurons;

XX RESULT 8
XX AAR86903
ID AAR86903 standard; Protein: 150 AA.
XX AC AAR86903;
XX DT 10-MAY-1996 (first entry)
XX DE Human BMP-9 polypeptide.
XX KW BMP-9; bone; cartilage; wound healing; liver; tissue repair.

AC AAR31374;
 XX
 DT 24-JUN-1993 (first entry)
 XX
 DE Human bone morphogenic protein-9 (BMP-9).
 XX
 KW bone formation; cartilage formation; wound healing; tissue repair;
 KW surgery; fracture treatment; Periodontal disease; osteoporosis;
 KW increase neuronal survival; transplantation; nerves; nervous system.
 XX
 OS Homo sapiens.
 XX
 PN WO9300432-A.
 XX
 PD 07-JAN-1993.
 XX
 PR 25-JUN-1992; 92WO-US05374.
 XX
 PR 25-JUN-1991; 91US-0720590.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Celeste AJ, Wozney JM;
 XX
 DR WPI; 1993-036379-04.
 N-PSDB; AAQ35244.
 PT New BMP-9 polypeptide(s) induce bone and cartilage formation -
 used for treating osteoporosis and fractures, healing wounds and
 increasing neuronal survival
 PT
 PS Example 2; Fig 3; 60pp; English.
 XX
 CC This sequence is human bone morphogenic protein-9. The protein can
 be used to induce bone and/or cartilage formation and in wound healing
 fractures, periodontal disease or osteoporosis. The protein can also
 increase neuronal survival and can be used in transplantation and
 treatment of conditions exhibiting a decrease in neuronal survival.
 XX
 SQ Sequence 150 AA:
 Query Match 45.2%; Score 619; DB 14; Length 150;
 Best Local Similarity 91.4%; Pred. No. 1.5e-55;
 Matches 112; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
 CC
 Oy 135 YTAGVPLARRRSTGASSKQKTSLRVNEFDIGWDSMILARKEYKAYECKGCFPLAD 194
 :| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 28 HVAAGSTLARRRSAGSKQKTSLRVNEFDIGWDSMILARKEYKAYECKGCFPLAD 87
 Qy 195 DVPPTKHAIVQTLVHVKFPTVKGACCVPTKLSPISIILYKDDMGVPTLYKHYEGMSVAEC 254
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 88 DVPPTKHAIVQTLVHVKFPTVKGACCVPTKLSPISIILYKDDMGVPTLYKHYEGMSVAEC 147
 Qy 255 GCR 257
 |||
 Db 148 GCR 150
 RESULT 11
 AAM51930 standard; protein; 110 AA.
 ID
 AC AAM51930;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human TSRbeta protein superfamily protein GDF2.
 XX
 KW Human; TGFbeta; transforming growth factor beta; mutant; antagonist;
 KW agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;
 formation; fibrosis; cirrhosis; osteopathic; antipsoriatic;
 KW antifibrotic; hepatotropic; vulnerary; GDF2.
 XX
 OS Homo sapiens.
 XX
 FN (SEBA/) SEBALD W.
 XX
 PI Sebald W, Nickel J;
 XX
 DR WPI; 2002-042559/06.
 XX
 PT New mutein of transforming growth factor-beta superfamily protein,
 PT useful for treating or preventing e.g. ectopic bone formation, competes
 for receptor binding
 XX
 PS Disclosure; Fig 6; 54pp; German.
 XX
 CC The present invention relates to muteins of a chain of a protein which,
 CC when in the form of a homodimer, has antagonistic or partial agonistic
 CC activity, and where the mutation results in the protein binding with low
 CC affinity to its receptor. The protein is a member of the transforming
 CC growth factor beta (TGFbeta) superfamily. The mutant sequences of the
 CC invention can be used in the treatment of diseases associated with the
 CC overexpression of TGFbeta family proteins, including ectopic bone
 CC formation, psoriasis, muscular atrophy, scar formation, fibrosis and
 CC cirrhosis. The present sequence is the human GDF2 protein.
 XX
 SQ Sequence 110 AA:
 Query Match 43.6%; Score 596; DB 23; Length 110;
 Best Local Similarity 96.4%; Pred. No. 2.3e-53;
 Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 CC
 Oy 148 STGASSHCOTSLRVNEFDIGWDSMILARKEYKAYECKGCFPLAD 207
 :| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 1 SAGAGSHCOTSLRVNEFDIGWDSMILARKEYKAYECKGCFPLADVVTPKHAIVOTL 60
 Qy 208 VHLKPFPTKVKACCVPTKLSPISIILYKDDMGVPTLYKHYEGMSVAEC 257
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 61 VHLKPFPTKVKACCVPTKLSPISIILYKDDMGVPTLYKHYEGMSVAEC 110
 RESULT 12
 AAR6200
 ID AAR6200 standard; Protein; 312 AA.
 XX
 AC AAR6200;
 XX
 DT 06-AUG-1995 (first entry)
 XX
 DE Part of bovine bone morphogenetic protein (BMP)-10.
 XX
 KW Bone morphogenetic protein; BMP; bone formation; cartilage;
 KW Periodontal disease; osteoporosis.
 XX
 OS Bos taurus.
 XX
 FN
 Key Location/Qualifiers
 FT 1..204
 FT Peptide
 FT /label= part of propeptide
 FT Protein
 FT 205..312
 FT /label= mature peptide
 XX
 PN WO9426893-A.
 XX
 PD 24-NOV-1994.
 XX

RESULT 14
 ID AAY92029 standard; Protein: 424 AA.
 AC AAY92029;
 DT 19-JUL-2000 (first entry)
 XX Human bone morphogenic protein-10 (BMP-10).
 XX human bone morphogenic protein-10; BMP-10; Vgrl growth factor; CKGF;
 KW mutant; cystine knot growth factor; hairpin loop; infertility.
 XX OS Homo sapiens.

Key Location/Qualifiers
 Misc-difference 1.326 /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
 FT Domain 327..353 /label= beta_hairpin_loop_1
 /note= "mutant optionally comprises one or more substitutions in these residues"
 FT Misc-difference 354..392 /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
 FT Domain 394..416 /label= beta_hairpin_loop_3
 /note= "mutant optionally comprises one or more substitutions in these residues"
 FT Misc-difference 417..424 /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
 FT Domain 394..416 /label= beta_hairpin_loop_3
 /note= "mutant optionally comprises one or more substitutions in these residues"
 FT Misc-difference 417..424 /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
 XX PN WO200117360-A1.
 XX PD 30-MAR-2000.
 XX PF 19-MAR-1999; 99W0-US05908.
 XX PR 22-SEP-1998; 98W0-US1972.
 XX PA (UWMA-) UNTV MARYLAND BALTIMORE.
 XX PI Weintraub BD, Szkludlinski MW;
 XX DR WPI; 2000-2B3585/24.
 XX PT New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g. hypothyroidism and thyroid cancer
 XX PS Claim 475; Page 310; 320pp; English.
 CC This is the wild type human bone morphogenic protein-10 (BMP-10). Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bioactivity. Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological activities of the CKGF.

CC Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.

RESULT 15
 ID AAY06304 standard; Protein: 421 AA.
 AC AAY06304;
 DT 31-AUG-1999 (first entry)
 XX DE Mouse pancreatic-derived factor PDF1.
 XX PD PDF1; pancreatic-derived factor; mouse; signal transduction; transforming growth factor-beta; pancreas; diabetes; therapy; KW diagnosis.
 XX OS Mus musculus.
 XX PA Key Location/Qualifiers
 FT Domain 320..333 /note= "core motif"
 XX PN WO9929719-A2.
 XX PD 17-JUN-1999.
 XX PT 09-DEC-1998; 99W0-US26165.
 XX PR 09-DEC-1997; 97US-0069071..
 XX PA (ONTIO-) ONTOGENY INC.
 XX PR Edlund H;
 XX WPI; 1999-3B85571/32.
 XX DR N-PSDB; AAX59115.
 XX PR New isolated pancreatic-derived factor polypeptides used for the treatment of a pancreatic disorder
 XX PS Claim 2; Page 82-84; 84pp; English.
 CC This sequence represents a novel mouse pancreatic-derived factor PDF1, as predicted from a cDNA clone (see AAX59115) obtained from foetal pancreatic bud cDNA. PDF1 shows homology to members of the

transforming growth factor-beta superfamily, especially BMP2a. Its expression in the developing pancreas indicates a role in the development of endodermal tissue and in particular in pancreas development. Experimental evidence indicates a functional role in signal transduction mediated by members of the TGF-beta superfamily. PDR1 and PDR2 (see AA06303) play a role in determining tissue fate and in maintenance of differentiated states. They can be used for the manufacture of medicaments for the treatment of a pancreatic disorder or to modulate growth and/or differentiation of pancreatic cells or stem cells capable of differentiating to pancreatic cells (claimed). PDR poly nucleotides, polypeptides and modulator compounds can be used for treating e.g. diabetes, liver disease, various cancers, leukemia, psoriasis, bone disease, fibroproliferative disorders, atherosclerosis, chronic inflammation, Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinocerebellar degeneration, disorders associated with connective tissue, e.g. de-differentiation of chondrocytes or osteocytes, vascular disorders which involve de-differentiation of endothelial tissue and smooth muscle cells, gastric ulcers characterized by degenerative changes in glandular cells, and renal conditions marked by failure to differentiate e.g. Wilms' tumors, to reform injured tissue, to improve grafting and morphology of transplanted tissue, e.g. PDR agonists and antagonists can be used in a differential manner to regulate different stages of organ repair after physical, chemical or pathological insult, in repair of pancreatic endocrine or exocrine function, cartilage repair, increasing bone density, liver repair subsequent to a partial hepatectomy, or to promote regeneration of lung tissue in the treatment of emphysema. Modulation of the function of PDR can be used in both cell culture and therapeutic methods involving generation and maintenance of beta cells and possibly also for non-pancreatic tissue, such as in controlling the development and maintenance of tissue from the digestive tract, spleen, lungs, and other organs which derive from the primitive gut. The products can also be used for treating endocrinopathies, sepsis (including malaria), congestive cardiac failure, hepatic and renal insufficiencies, various genetic abnormalities of metabolism, and exogenous toxins (such as alcohol). PDR therapeutics can also be used in the treatment of hyperproliferative vascular disorders, e.g. smooth muscle hyperplasia (such as atherosclerosis) or restenosis, as well as other disorders characterized by fibrosis, e.g. rheumatoid arthritis, insulin dependent diabetes mellitus, glomerulonephritis, cirrhosis, and scleroderma, particularly proliferative disorders in which loss of a TGF-beta autocrine or paracrine signaling is implicated. They can also be used to modulate spermatogenesis and to treat disorders of the female reproductive system which lead to infertility including polycystic ovarian syndrome. The products can also be used for detection, diagnosis and drug screening.

SQ Sequence 421 AA:

Query Match 37.1%; Score 508; DB 20; Length 421;
Best Local Similarity 42.5%; Pred. No. 1.8e 43%;
Matches 114; Conservative 50; Mismatches 78; Indels 26; Gaps 10;

Qy 1 DYLDSSETWDQATGKTPLVSDI--RDEGEGTEVLSAVKRMVADSTINNKLEVNO 58
Db 169 EVLSSADGSEER-SMLVLUVSTBLYGTSNENETFDVDTARRWQSGPST-HOLEHIE 225
Qy 59 SHRESCD---TLDISUPPGKNUPLPFVWFSNDSNGKETRDLKLKEMIGHEQETMLV 113
Db 226 SROQNAEDTGRGOLLEIDOMSAOKHDPULLWFSDDDSN-DREOK-EELNBULITHEODDLD 283
Qy 114 TAKAKNAYOGAGE---SOEEEGLDGYTAVGFLPALARRKSTGASSICQKTSLRVNFEDIGW 169
Db 284 SDA--FFSCPDEEALLQMRNMIDSSA-----RIRMAKGWYCKKPPLYDFKEIGW 334
Qy 170 DSWTIAPKKEYDAYECKGCCFFPLADDVPTKTHATQTVLNUKFPKVKGACCVPTKTSPI 229
Db 335 DSWTIAPKKEYAVECGRGVNYPLAHLIPTKHAIQALVILKNSQASKRACCPKPTKLDPI 394
Qy 230 SILYKDDMGVPTLKHYEGMSVAECGCR 257

Db 395 SIVYL-DKGWVTPKFVYEGMAVSECGR 421
Search completed: April 2, 2003, 14:49:34
Job time : 77 secs